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(54) Title: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as colon cancer, are disclosed. Compositions may comprise one or more colon tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a colon tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as colon cancer. Diagnostic methods based on detecting a colon tumor protein, or mRNA encoding such a protein, in a sample are also provided.

COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

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The present invention relates generally to therapy and diagnosis of cancer, such as colon cancer. The invention is more specifically related to polypeptides comprising at least a portion of a colon tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of colon cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Colon cancer is the second most frequently diagnosed malignancy in the United States as well as the second most common cause of cancer death. An estimated 95,600 new cases of colon cancer will be diagnosed in 1998, with an estimated 47,700 deaths. The five-year survival rate for patients with colorectal cancer detected in an early localized stage is 92%; unfortunately, only 37% of colorectal cancer is diagnosed at this stage. The survival rate drops to 64% if the cancer is allowed to spread to adjacent organs or lymph nodes, and to 7% in patients with distant metastases.

The prognosis of colon cancer is directly related to the degree of penetration of the tumor through the bowel wall and the presence or absence of nodal involvement, consequently, early detection and treatment are especially important. Currently, diagnosis is aided by the use of screening assays for fecal occult blood, sigmoidoscopy, colonoscopy and double contrast barium enemas. Treatment

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regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. Recurrence following surgery (the most common form of therapy) is a major problem and is often the ultimate cause of death. In spite of considerable research into therapies for the disease, colon cancer remains difficult to diagnose and treat. In spite of considerable research into therapies for these and other cancers, colon cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

10 SUMMARY OF THE INVENTION

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Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as colon cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a colon tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-121, 123-197, 205-630, 632-684, 686, 690-691 and 694-1081; (b) variants of a sequence recited in SEQ ID NO: 1-121, 123-197, 205-630 and 632-684, 686, 690-691 and 694-1081; and (c) complements of a sequence of (a) or (b).

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a colon tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

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Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a colon tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

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Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a colon tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

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Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a colon tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a colon tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expresses such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be colon cancer.

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The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

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The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a colon tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a colon tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount

detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached figures. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

- SEQ ID NO: 1 is a first determined cDNA sequence for Contig 1, showing homology to Neutrophil Gelatinase Associated Lipocalin.
- SEQ ID NO: 2 is the determined cDNA sequence for Contig 2, showing no significant homology to any known genes.
 - SEQ ID NO: 3 is the determined cDNA sequence for Contig 4, showing homology to Carcinoembryonic antigen.
 - SEQ ID NO: 4 is the determined cDNA sequence for Contig 5, showing homology to Carcinoembryonic antigen.
- SEQ ID NO: 5 is the determined cDNA sequence for Contig 9, showing homology to Carcinoembryonic antigen.
 - SEQ ID NO: 6 is the determined cDNA sequence for Contig 52, showing homology to Carcinoembryonic antigen.
- SEQ ID NO: 7 is the determined cDNA sequence for Contig 6, showing homology to Villin.
 - SEQ ID NO: 8 is the determined cDNA sequence for Contig 8, showing no significant homology to any known genes.
 - SEQ ID NO: 9 is the determined cDNA sequence for Contig 10, showing homology to Transforming Growth Factor (BIGH3).

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SEQ ID NO: 10 is the determined cDNA sequence for Contig 19, showing homology to Transforming Growth Factor (BIGH3).

SEQ ID NO: 11 is the determined cDNA sequence for Contig 21, showing homology to Transforming Growth Factor (BIGH3).

5 SEQ ID NO: 12 is the determined cDNA sequence for Contig 11, showing homology to CO-029.

SEQ ID NO: 13 is the determined cDNA sequence for Contig 55, showing homology to CO-029.

SEQ ID NO: 14 is the determined cDNA sequence for Contig 12, showing homology to Chromosome 17, clone hRPC.1171_I_10, also referred to as C798P.

SEQ ID NO: 15 is the determined cDNA sequence for Contig 13, showing no significant homology to any known gene.

SEQ ID NO: 16 is the determined cDNA sequence for Contig 14, also referred to as 14261, showing no significant homology to any known gene.

SEQ ID NO: 17 is the determined cDNA sequence for Contig 15, showing homology to Ets-Related Transcription Factor (ERT).

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SEQ ID NO: 18 is the determined cDNA sequence for Contig 16, showing homology to Chromosome 5, PAC clone 228g9 (LBNL H142).

SEQ ID NO: 19 is the determined cDNA sequence for Contig 24, showing homology to Chromosome 5, PAC clone 228g9 (LBNL H142).

SEQ ID NO: 20 is the determined cDNA sequence for Contig 17, showing homology to Cytokeratin.

SEQ ID NO: 21 is the determined cDNA sequence for Contig 18, showing homology to L1-Cadherin.

SEQ ID NO: 22 is the determined cDNA sequence for Contig 20, showing no significant homology to any known gene.

SEQ ID NO: 23 is the determined cDNA sequence for Contig 22, showing homology to Burnetanide-sensitive Na-K-Cl cotransporter (NKCCl).

SEQ ID NO: 24 is the determined cDNA sequence for Contig 23, showing no significant homology to any known gene.

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SEQ ID NO: 25 is the determined cDNA sequence for Contig 25, showing homology to Macrophage Inflammatory Protein 3 alpha.

SEQ ID NO: 26 is the determined cDNA sequence for Contig 26, showing homology to Laminin.

5 SEQ ID NO: 27 is the determined cDNA sequence for Contig 48, showing homology to Laminin.

SEQ ID NO: 28 is the determined cDNA sequence for Contig 27, showing homology to Mytobularin (MTM1).

SEQ ID NO: 29 is the determined cDNA sequence for Contig 28, showing homology to Chromosome 16 BAC clone CIT987SK-A-363E6.

SEQ ID NO: 30 is the determined cDNA sequence for Contig 29, also referred to as C751P and 14247, showing no significant homology to any known gene, but partial homology to Rat GSK-3β-interacting protein Axil homolog.

SEQ ID NO: 31 is the determined cDNA sequence for Contig 30, showing homology to Zinc Finger Transcription Factor (ZNF207).

SEQ ID NO: 32 is the determined cDNA sequence for Contig 31, showing no significant homology to any known gene, but partial homology to Mus musculus GOB-4 homolog.

SEQ ID NO: 33 is the determined cDNA sequence for Contig 35, showing no significant homology to any known gene, but partial homology to Mus musculus GOB-4 homolog.

SEQ ID NO: 34 is the determined cDNA sequence for Contig 32, showing no significant homology to any known gene.

SEQ ID NO: 35 is the determined cDNA sequence for Contig 34, showing homology to Desmoglein 2.

SEQ ID NO: 36 is the determined cDNA sequence for Contig 36, showing no significant homology to any known gene.

SEQ ID NO: 37 is the determined cDNA sequence for Contig 37, showing homology to Putative Transmembrane Protein.

SEQ ID NO: 38 is the determined cDNA sequence for Contig 38, also referred to as C796P and 14219, showing no significant homology to any known gene.

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SEQ ID NO: 39 is the determined cDNA sequence for Contig 40, showing homology to Nonspecific Cross-reacting Antigen.

SEQ ID NO: 40 is the determined cDNA sequence for Contig 41, also referred to as C799P and 14308, showing no significant homology to any known gene.

SEQ ID NO: 41 is the determined cDNA sequence for Contig 42, also referred to as C794P and 14309, showing no significant homology to any known gene.

SEQ ID NO: 42 is the determined cDNA sequence for Contig 43, showing homology to Chromosome 1 specific transcript KIAA0487.

SEQ ID NO: 43 is the determined cDNA sequence for Contig 45, showing 10 homology to hMCM2.

SEQ ID NO: 44 is the determined cDNA sequence for Contig 46, showing homology to ETS2.

SEQ ID NO: 45 is the determined cDNA sequence for Contig 49, showing homology to Pump-1.

SEQ ID NO: 46 is the determined cDNA sequence for Contig 50, also referred to as C792P and 18323, showing no significant homology to any known gene.

SEQ ID NO: 47 is the determined cDNA sequence for Contig 51, also referred to as C795P and 14317, showing no significant homology to any known gene.

SEQ ID NO: 48 is the determined cDNA sequence for 11092, showing no significant homology to any known gene.

SEQ ID NO: 49 is the determined cDNA sequence for 11093, showing no significant homology to any known gene.

SEQ ID NO: 50 is the determined cDNA sequence for 11094, showing homology Human Putative Enterocyte Differentiation Protein.

SEQ ID NO: 51 is the determined cDNA sequence for 11095, showing homology to Human Transcriptional Corepressor hKAP1/TIF1B mRNA.

SEQ ID NO: 52 is the determined cDNA sequence for 11096, showing no significant homology to any known gene.

SEQ ID NO: 53 is the determined cDNA sequence for 11097, showing homology to Human Nonspecific Antigen.

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SEQ ID NO: 54 is the determined cDNA sequence for 11098, showing no significant homology to any known gene.

SEQ ID NO: 55 is the determined cDNA sequence for 11099, showing homology to Human Pancreatic Secretory Inhibitor (PST) mRNA.

SEQ ID NO: 56 is the determined cDNA sequence for 11186, showing homology to Human Pancreatic Secretory Inhibitor (PST) mRNA.

SEQ ID NO: 57 is the determined cDNA sequence for 11101, showing homology to Human Chromosome X.

SEQ ID NO: 58 is the determined cDNA sequence for 11102, showing homology to Human Chromosome X.

SEQ ID NO: 59 is the determined cDNA sequence for 11103, showing no significant homology to any known gene.

SEQ ID NO: 60 is the determined cDNA sequence for 11174, showing no significant homology to any known gene.

SEQ ID NO: 61 is the determined cDNA sequence for 11104, showing homology to Human mRNA for KIAA0154.

SEQ ID NO: 62 is the determined cDNA sequence for 11105, showing homology to Human Apurinic/Apyrimidinic Endonuclease (hap1)mRNA.

SEQ ID NO: 63 is the determined cDNA sequence for 11106, showing homology to Human Chromosome 12p13.

SEQ ID NO: 64 is the determined cDNA sequence for 11107, showing homology to Human 90 kDa Heat Shock Protein.

SEQ ID NO: 65 is the determined cDNA sequence for 11108, showing no significant homology to any known gene.

SEQ ID NO: 66 is the determined cDNA sequence for 11112, showing no significant homology to any known gene.

SEQ ID NO: 67 is the determined cDNA sequence for 11115, showing no significant homology to any known gene.

SEQ ID NO: 68 is the determined cDNA sequence for 11117, showing no significant homology to any known gene.

SEQ ID NO: 69 is the determined cDNA sequence for 11118, showing no significant homology to any known gene.

SEQ ID NO: 70 is the determined cDNA sequence for 11119, showing homology to Human Elongation Factor 1-alpha.

SEQ ID NO: 71 is the determined cDNA sequence for 11121, showing homology to Human Lamin B Receptor (LBR) mRNA.

SEQ ID NO: 72 is the determined cDNA sequence for 11122, showing homology to H. sapiens mRNA for Novel Glucocorticoid.

SEQ ID NO: 73 is the determined cDNA sequence for 11123, showing homology to H. sapiens mRNA for snRNP protein B.

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SEQ ID NO: 74 is the determined cDNA sequence for 11124, showing homology to Human Cisplatin Resistance Associated Beta-protein.

SEQ ID NO: 75 is the determined cDNA sequence for 11127, showing homology to M. musculus Calumenin mRNA.

SEQ ID NO: 76 is the determined cDNA sequence for 11128, showing homology to Human ras-related small GTP binding protein.

SEQ ID NO: 77 is the determined cDNA sequence for 11130, showing homology to Human Cosmid U169d2.

SEQ ID NO: 78 is the determined cDNA sequence for 11131, showing homology to H. sapiens mRNA for protein homologous to Elongation 1-g.

SEQ ID NO: 79 is the determined cDNA sequence for 11134, showing no significant homology to any known gene.

SEQ ID NO: 80 is the determined cDNA sequence for 11135, showing homology to H. sapiens Nieman-Pick (NPC1) mRNA.

SEQ ID NO: 81 is the determined cDNA sequence for 11137, showing homology to H. sapiens mRNA for Niecin b-chain.

SEQ ID NO: 82 is the determined cDNA sequence for 11138, showing homology to Human Endogenous Retroviral Protease mRNA.

SEQ ID NO: 83 is the determined cDNA sequence for 11139, showing homology to H. sapiens mRNA for DMBT1 protein.

SEQ ID NO: 84 is the determined cDNA sequence for 11140, showing homology to H. sapiens ras GTPase activating-like protein.

SEQ ID NO: 85 is the determined cDNA sequence for 11143, showing homology to Human Acidic Ribosomal Phosphoprotein PO mRNA.

5 SEQ ID NO: 86 is the determined cDNA sequence for 11144, showing homology to H. sapiens U21 mRNA.

SEQ ID NO: 87 is the determined cDNA sequence for 11145, showing homology to Human GTP-binding protein.

SEQ ID NO: 88 is the determined cDNA sequence for 11148, showing homology to H. sapiens U21 mRNA.

SEQ ID NO: 89 is the determined cDNA sequence for 11151, showing no significant homology to any known gene.

SEQ ID NO: 90 is the determined cDNA sequence for 11154, showing no significant homology to any known gene.

SEQ ID NO: 91 is the determined cDNA sequence for 11156, showing homology to H. sapiens Ribosomal Protein L27.

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SEQ ID NO: 92 is the determined cDNA sequence for 11157, showing homology to H. sapiens Ribosomal Protein L27.

SEQ ID NO: 93 is the determined cDNA sequence for 11158, showing no significant homology to any known gene.

SEQ ID NO: 94 is the determined cDNA sequence for 11162, showing homology to Ag-X antigen.

SEQ ID NO: 95 is the determined cDNA sequence for 11164, showing homology to H. sapiens mRNA for Signal Recognition Protein sub14.

SEQ ID NO: 96 is the determined cDNA sequence for 11165, showing homology to Human PAC 204e5/127h14.

SEQ ID NO: 97 is the determined cDNA sequence for 11166, showing homology to Human mRNA for KIAA0108.

SEQ ID NO: 98 is the determined cDNA sequence for 11167, showing homology to H. sapiens mRNA for Neutrophil Gelatinase assct. Lipocalin.

SEQ ID NO: 99 is the determined cDNA sequence for 11168, showing no significant homology to any known gene.

SEQ ID NO: 100 is the determined cDNA sequence for 11172, showing no significant homology to any known gene.

SEQ ID NO: 101 is the determined cDNA sequence for 11175, showing no significant homology to any known gene.

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SEQ ID NO: 102 is the determined cDNA sequence for 11176, showing homology to Human maspin mRNA.

SEQ ID NO: 103 is the determined cDNA sequence for 11177, showing homology to Human Carcinoembryonic Antigen.

SEQ ID NO: 104 is the determined cDNA sequence for 11178, showing homology to Human A-Tubulin mRNA.

SEQ ID NO: 105 is the determined cDNA sequence for 11179, showing homology to Human mRNA for proton-ATPase-like protein.

SEQ ID NO: 106 is the determined cDNA sequence for 11180, showing homology to Human HepG2 3' region cDNA clone hmd.

SEQ ID NO: 107 is the determined cDNA sequence for 11182, showing homology to Human MHC homologous to Chicken B-Complex Protein.

SEQ ID NO: 108 is the determined cDNA sequence for 11183, showing homology to Human High Mobility Group Box (SSRP1) mRNA.

SEQ ID NO: 109 is the determined cDNA sequence for 11184, showing no significant homology to any known gene.

SEQ ID NO: 110 is the determined cDNA sequence for 11185, showing no significant homology to any known gene.

SEQ ID NO: 111 is the determined cDNA sequence for 11187, showing no significant homology to any known gene.

SEQ ID NO: 112 is the determined cDNA sequence for 11190, showing homology to Human Replication Protein A 70kDa.

SEQ ID NO: 113 is the determined cDNA sequence for Contig 47, also referred to as C797P, showing homology to Human Chromosome X clone bWXD342.

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SEQ ID NO: 114 is the determined cDNA sequence for Contig 7, showing homology to Equilibrative Nucleoside Transporter 2 (ent2).

SEQ ID NO: 115 is the determined cDNA sequence for 14235.1, also referred to as C791P, showing homology to H. sapiens chromosome 21 derived BAC containing ets-2 gene.

SEQ ID NO: 116 is the determined cDNA sequence for 14287.2, showing no significant homology to any known gene, but some degree of homology to Putative Transmembrane Protein.

SEQ ID NO: 117 is the determined cDNA sequence for 14233.1, also referred to as Contig 48, showing no significant homology to any known gene.

SEQ ID NO: 118 is the determined cDNA sequence for 14298.2, also referred to as C793P, showing no significant homology to any known gene.

SEQ ID NO: 119 is the determined cDNA sequence for 14372, also referred to as Contig 44, showing no significant homology to any known gene.

SEQ ID NO: 120 is the determined cDNA sequence for 14295, showing homology to secreted cement gland protein XAG-2 homolog.

SEQ ID NO: 121 is the determined full-length cDNA sequence for a clone showing homology to Beta IG-H3.

SEQ ID NO: 122 is the predicted amino acid sequence for the clone of SEQ ID 20 NO: 121.

SEQ ID NO: 123 is a longer determined cDNA sequence for C751P.

SEQ ID NO: 124 is a longer determined cDNA sequence for C791P.

SEQ ID NO: 125 is a longer determined cDNA sequence for C792P.

SEQ ID NO: 126 is a longer determined cDNA sequence for C793P.

SEQ ID NO: 127 is a longer determined cDNA sequence for C794P.

SEQ ID NO: 128 is a longer determined cDNA sequence for C795P.

SEO ID NO: 129 is a longer determined cDNA sequence for C796P.

SEQ ID NO: 130 is a longer determined cDNA sequence for C797P.

SEQ ID NO: 131 is a longer determined cDNA sequence for C798P.

SEQ ID NO: 132 is a longer determined cDNA sequence for C799P.

25

SEQ ID NO: 133 is a first partial determined cDNA sequence for CoSub-3 (also known as 23569).

SEQ ID NO: 134 is a second partial determined cDNA sequence for CoSub-3 (also known as 23569).

5 SEQ ID NO: 135 is a first partial determined cDNA sequence for CoSub-13 (also known as 23579).

SEQ ID NO: 136 is a second partial determined cDNA sequence for CoSub-13 (also known as 23579).

SEQ ID NO: 137 is the determined cDNA sequence for CoSub-17 (also known as 23583).

SEQ ID NO: 138 is the determined cDNA sequence for CoSub-19 (also known as 23585).

SEQ ID NO: 139 is the determined cDNA sequence for CoSub-22 (also known as 23714).

SEQ ID NO: 140 is the determined cDNA sequence for CoSub-23 (also known as 23715).

SEQ ID NO: 141 is the determined cDNA sequence for CoSub-26 (also known as 23717).

SEQ ID NO: 142 is the determined cDNA sequence for CoSub-33 (also known as 23724).

SEQ ID NO: 143 is the determined cDNA sequence for CoSub-34 (also known as 23725).

SEQ ID NO: 144 is the determined cDNA sequence for CoSub-35 (also known as 23726).

SEQ ID NO: 145 is the determined cDNA sequence for CoSub-37 (also known as 23728).

SEQ ID NO: 146 is the determined cDNA sequence for CoSub-39 (also known as 23730).

SEQ ID NO: 147 is the determined cDNA sequence for CoSub-42 (also known as 23766).

16

SEQ ID NO: 148 is the determined cDNA sequence for CoSub-44 (also known as 23768).

SEQ ID NO: 149 is the determined cDNA sequence for CoSub-47 (also known as 23771).

5 SEQ ID NO: 150 is the determined cDNA sequence for CoSub-54 (also known as 23778).

SEQ ID NO: 151 is the determined cDNA sequence for CoSub-55 (also known as 23779).

SEQ ID NO: 152 is the determined cDNA sequence for CT1 (also known as 10 24099).

SEQ ID NO: 153 is the determined cDNA sequence for CT2 (also known as 24100).

SEQ ID NO: 154 is the determined cDNA sequence for CT3 (also known as 24101).

SEQ ID NO: 155 is the determined cDNA sequence for CT6 (also known as 24104).

SEQ ID NO: 156 is the determined cDNA sequence for CT7 (also known as 24105).

SEQ ID NO: 157 is the determined cDNA sequence for CT12 (also known as 20 24110).

SEQ ID NO: 158 is the determined cDNA sequence for CT13 (also known as 24111).

SEQ ID NO: 159 is the determined cDNA sequence for CT14 (also known as 24112).

25 SEQ ID NO: 160 is the determined cDNA sequence for CT15 (also known as 24113).

SEQ ID NO: 161 is the determined cDNA sequence for CT17 (also known as 24115).

SEQ ID NO: 162 is the determined cDNA sequence for CT18 (also known as 24116).

SEQ ID NO: 163 is the determined cDNA sequence for CT22 (also known as 23848).

SEQ ID NO: 164 is the determined cDNA sequence for CT24 (also known as 23849).

5 SEQ ID NO: 165 is the determined cDNA sequence for CT31 (also known as 23854).

SEQ ID NO: 166 is the determined cDNA sequence for CT34 (also known as 23856).

SEQ ID NO: 167 is the determined cDNA sequence for CT37 (also known as 10 23859).

SEQ ID NO: 168 is the determined cDNA sequence for CT39 (also known as 23860).

SEQ ID NO: 169 is the determined cDNA sequence for CT40 (also known as 23861).

15 SEQ ID NO: 170 is the determined cDNA sequence for CT51 (also known as 24130).

SEQ ID NO: 171 is the determined cDNA sequence for CT53 (also known as 24132).

SEQ ID NO: 172 is the determined cDNA sequence for CT63 (also known as 20 24595).

SEQ ID NO: 173 is the determined cDNA sequence for CT88 (also known as 24608).

SEQ ID NO: 174 is the determined cDNA sequence for CT92 (also known as 24800).

SEQ ID NO: 175 is the determined cDNA sequence for CT94 (also known as 24802).

SEQ ID NO: 176 is the determined cDNA sequence for CT102 (also known as 24805).

SEQ ID NO: 177 is the determined cDNA sequence for CT103 (also known as 24806).

SEQ ID NO: 178 is the determined cDNA sequence for CT111 (also known as

25520).

SEQ ID NO: 179 is the determined cDNA sequence for CT118 (also known as 25522).

5 SEQ ID NO: 180 is the determined cDNA sequence for CT121 (also known as 25523).

SEQ ID NO: 181 is the determined cDNA sequence for CT126 (also known as 25527).

SEQ ID NO: 182 is the determined cDNA sequence for CT135 (also known as 10 25534).

SEQ ID NO: 183 is the determined cDNA sequence for CT140 (also known as 25537).

SEQ ID NO: 184 is the determined cDNA sequence for CT145 (also known as 25542).

15 SEQ ID NO: 185 is the determined cDNA sequence for CT147 (also known as 25543).

SEQ ID NO: 186 is the determined cDNA sequence for CT148 (also known as 25544).

SEQ ID NO: 187 is the determined cDNA sequence for CT502 (also known as 20 26420).

SEQ ID NO: 188 is the determined cDNA sequence for CT507 (also known as 26425).

SEQ ID NO: 189 is the determined cDNA sequence for CT521 (also known as 27366).

25 SEQ ID NO: 190 is the determined cDNA sequence for CT544 (also known as 27375).

SEQ ID NO: 191 is the determined cDNA sequence for CT577 (also known as 27385).

SEQ ID NO: 192 is the determined cDNA sequence for CT580 (also known as 30 27387).

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SEQ ID NO: 193 is the determined cDNA sequence for CT594 (also known as 27540).

SEQ ID NO: 194 is the determined cDNA sequence for CT606 (also known as 27547).

5 SEQ ID NO: 195 is the determined cDNA sequence for CT607 (also known as 27548).

SEQ ID NO: 196 is the determined cDNA sequence for CT599 (also known as 27903).

SEQ ID NO: 197 is the determined cDNA sequence for CT632 (also known as 10 27922).

SEQ ID NO: 198 is the predicted amino acid sequence for CT502 (SEQ ID NO: 187).

SEQ ID NO: 199 is the predicted amino acid sequence for CT507 (SEQ ID NO: 188).

SEQ ID NO: 200 is the predicted amino acid sequence for CT521 (SEQ ID NO: 189).

SEQ ID NO: 201 is the predicted amino acid sequence for CT544 (SEQ ID NO: 190).

SEQ ID NO: 202 is the predicted amino acid sequence for CT606 (SEQ ID 20 NO: 194).

SEQ ID NO: 203 is the predicted amino acid sequence for CT607 (SEQ ID NO: 195).

SEQ ID NO: 204 is the predicted amino acid sequence for CT632 (SEQ ID NO: 197).

SEQ ID NO: 205 is the determined cDNA sequence for clone 25244.

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SEQ ID NO: 206 is the determined cDNA sequence for clone 25245.

SEQ ID NO: 207 is the determined cDNA sequence for clone 25246.

SEQ ID NO: 208 is the determined cDNA sequence for clone 25248.

SEQ ID NO: 209 is the determined cDNA sequence for clone 25249.

SEQ ID NO: 210 is the determined cDNA sequence for clone 25250.

SEQ ID NO: 211 is the determined cDNA sequence for clone 25251.

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SEQ ID NO: 212 is the determined cDNA sequence for clone 25252. SEQ ID NO: 213 is the determined cDNA sequence for clone 25253. SEQ ID NO: 214 is the determined cDNA sequence for clone 25254. SEQ ID NO: 215 is the determined cDNA sequence for clone 25255. SEQ ID NO: 216 is the determined cDNA sequence for clone 25256. SEQ ID NO: 217 is the determined cDNA sequence for clone 25257. SEQ ID NO: 218 is the determined cDNA sequence for clone 25259. SEQ ID NO: 219 is the determined cDNA sequence for clone 25260. SEQ ID NO: 220 is the determined cDNA sequence for clone 25261. SEQ ID NO: 221 is the determined cDNA sequence for clone 25262. SEQ ID NO: 222 is the determined cDNA sequence for clone 25263. SEQ ID NO: 223 is the determined cDNA sequence for clone 25264. SEQ ID NO: 224 is the determined cDNA sequence for clone 25265. SEQ ID NO: 225 is the determined cDNA sequence for clone 25266. SEQ ID NO: 226 is the determined cDNA sequence for clone 25267. SEQ ID NO: 227 is the determined cDNA sequence for clone 25268. SEQ ID NO: 228 is the determined cDNA sequence for clone 25269. SEQ ID NO: 229 is the determined cDNA sequence for clone 25271. SEQ ID NO: 230 is the determined cDNA sequence for clone 25272. SEO ID NO: 231 is the determined cDNA sequence for clone 25273. 20 SEQ ID NO: 232 is the determined cDNA sequence for clone 25274. SEQ ID NO: 233 is the determined cDNA sequence for clone 25275. SEQ ID NO: 234 is the determined cDNA sequence for clone 25276. SEQ ID NO: 235 is the determined cDNA sequence for clone 25277. SEQ ID NO: 236 is the determined cDNA sequence for clone 25278. 25 SEQ ID NO: 237 is the determined cDNA sequence for clone 25280. SEQ ID NO: 238 is the determined cDNA sequence for clone 25281. SEQ ID NO: 239 is the determined cDNA sequence for clone 25282. SEQ ID NO: 240 is the determined cDNA sequence for clone 25283. SEQ ID NO: 241 is the determined cDNA sequence for clone 25284. 30 SEQ ID NO: 242 is the determined cDNA sequence for clone 25285.

SEQ ID NO: 243 is the determined cDNA sequence for clone 25286. SEQ ID NO: 244 is the determined cDNA sequence for clone 25287. SEQ ID NO: 245 is the determined cDNA sequence for clone 25288. SEQ ID NO: 246 is the determined cDNA sequence for clone 25289. SEQ ID NO: 247 is the determined cDNA sequence for clone 25290. 5 SEQ ID NO: 248 is the determined cDNA sequence for clone 25291. SEQ ID NO: 249 is the determined cDNA sequence for clone 25292. SEQ ID NO: 250 is the determined cDNA sequence for clone 25293. SEQ ID NO: 251 is the determined cDNA sequence for clone 25294. SEO ID NO: 252 is the determined cDNA sequence for clone 25295. 10 SEQ ID NO: 253 is the determined cDNA sequence for clone 25296. SEQ ID NO: 254 is the determined cDNA sequence for clone 25297. SEQ ID NO: 255 is the determined cDNA sequence for clone 25418. SEO ID NO: 256 is the determined cDNA sequence for clone 25419. SEQ ID NO: 257 is the determined cDNA sequence for clone 25420. 15 SEQ ID NO: 258 is the determined cDNA sequence for clone 25421. SEQ ID NO: 259 is the determined cDNA sequence for clone 25422. SEQ ID NO: 260 is the determined cDNA sequence for clone 25423. SEQ ID NO: 261 is the determined cDNA sequence for clone 25424. SEQ ID NO: 262 is the determined cDNA sequence for clone 25426. 20 SEQ ID NO: 263 is the determined cDNA sequence for clone 25427. SEQ ID NO: 264 is the determined cDNA sequence for clone 25428. SEQ ID NO: 265 is the determined cDNA sequence for clone 25429. SEQ ID NO: 266 is the determined cDNA sequence for clone 25430. 25 SEQ ID NO: 267 is the determined cDNA sequence for clone 25431. SEQ ID NO: 268 is the determined cDNA sequence for clone 25432. SEQ ID NO: 269 is the determined cDNA sequence for clone 25433. SEQ ID NO: 270 is the determined cDNA sequence for clone 25434. SEQ ID NO: 271 is the determined cDNA sequence for clone 25435. SEQ ID NO: 272 is the determined cDNA sequence for clone 25436. 30 SEQ ID NO: 273 is the determined cDNA sequence for clone 25437.

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SEQ ID NO: 274 is the determined cDNA sequence for clone 25438. SEQ ID NO: 275 is the determined cDNA sequence for clone 25439. SEQ ID NO: 276 is the determined cDNA sequence for clone 25440. SEQ ID NO: 277 is the determined cDNA sequence for clone 25441. 5 SEQ ID NO: 278 is the determined cDNA sequence for clone 25442. SEQ ID NO: 279 is the determined cDNA sequence for clone 25443. SEQ ID NO: 280 is the determined cDNA sequence for clone 25444. SEQ ID NO: 281 is the determined cDNA sequence for clone 25445. SEQ ID NO: 282 is the determined cDNA sequence for clone 25446. 10 SEQ ID NO: 283 is the determined cDNA sequence for clone 25447. SEQ ID NO: 284 is the determined cDNA sequence for clone 25448. SEQ ID NO: 285 is the determined cDNA sequence for clone 25844. SEQ ID NO: 286 is the determined cDNA sequence for clone 25845. SEQ ID NO: 287 is the determined cDNA sequence for clone 25846. 15 SEQ ID NO: 288 is the determined cDNA sequence for clone 25847. SEQ ID NO: 289 is the determined cDNA sequence for clone 25848. SEQ ID NO: 290 is the determined cDNA sequence for clone 25850. SEQ ID NO: 291 is the determined cDNA sequence for clone 25851. SEQ ID NO: 292 is the determined cDNA sequence for clone 25852. SEQ ID NO: 293 is the determined cDNA sequence for clone 25853. 20 SEQ ID NO: 294 is the determined cDNA sequence for clone 25854. SEQ ID NO: 295 is the determined cDNA sequence for clone 25855. SEQ ID NO: 296 is the determined cDNA sequence for clone 25856. SEQ ID NO: 297 is the determined cDNA sequence for clone 25857. SEQ ID NO: 298 is the determined cDNA sequence for clone 25858. 25 SEQ ID NO: 299 is the determined cDNA sequence for clone 25859. SEQ ID NO: 300 is the determined cDNA sequence for clone 25860. SEQ ID NO: 301 is the determined cDNA sequence for clone 25861. SEQ ID NO: 302 is the determined cDNA sequence for clone 25862. SEQ ID NO: 303 is the determined cDNA sequence for clone 25863. 30 SEQ ID NO: 304 is the determined cDNA sequence for clone 25864.

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SEQ ID NO: 305 is the determined cDNA sequence for clone 25865. SEQ ID NO: 306 is the determined cDNA sequence for clone 25866. SEQ ID NO: 307 is the determined cDNA sequence for clone 25867. SEQ ID NO: 308 is the determined cDNA sequence for clone 25868. SEQ ID NO: 309 is the determined cDNA sequence for clone 25869. SEQ ID NO: 310 is the determined cDNA sequence for clone 25870. SEQ ID NO: 311 is the determined cDNA sequence for clone 25871. SEQ ID NO: 312 is the determined cDNA sequence for clone 25872. SEQ ID NO: 313 is the determined cDNA sequence for clone 25873. SEQ ID NO: 314 is the determined cDNA sequence for clone 25875. SEQ ID NO: 315 is the determined cDNA sequence for clone 25876. SEQ ID NO: 316 is the determined cDNA sequence for clone 25877. SEQ ID NO: 317 is the determined cDNA sequence for clone 25878. SEQ ID NO: 318 is the determined cDNA sequence for clone 25879. SEQ ID NO: 319 is the determined cDNA sequence for clone 25880. SEQ ID NO: 320 is the determined cDNA sequence for clone 25881. SEQ ID NO: 321 is the determined cDNA sequence for clone 25882. SEQ ID NO: 322 is the determined cDNA sequence for clone 25883. SEQ ID NO: 323 is the determined cDNA sequence for clone 25884. SEQ ID NO: 324 is the determined cDNA sequence for clone 25885. SEQ ID NO: 325 is the determined cDNA sequence for clone 25886. SEQ ID NO: 326 is the determined cDNA sequence for clone 25887. SEQ ID NO: 327 is the determined cDNA sequence for clone 25888. SEQ ID NO: 328 is the determined cDNA sequence for clone 25889. SEQ ID NO: 329 is the determined cDNA sequence for clone 25890. SEQ ID NO: 330 is the determined cDNA sequence for clone 25892. SEQ ID NO: 331 is the determined cDNA sequence for clone 25894. SEQ ID NO: 332 is the determined cDNA sequence for clone 25895. SEQ ID NO: 333 is the determined cDNA sequence for clone 25896. SEQ ID NO: 334 is the determined cDNA sequence for clone 25897. SEQ ID NO: 335 is the determined cDNA sequence for clone 25899.

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SEQ ID NO: 336 is the determined cDNA sequence for clone 25900. SEQ ID NO: 337 is the determined cDNA sequence for clone 25901. SEQ ID NO: 338 is the determined cDNA sequence for clone 25902. SEQ ID NO: 339 is the determined cDNA sequence for clone 25903. SEQ ID NO: 340 is the determined cDNA sequence for clone 25904. 5 SEO ID NO: 341 is the determined cDNA sequence for clone 25906. SEQ ID NO: 342 is the determined cDNA sequence for clone 25907. SEQ ID NO: 343 is the determined cDNA sequence for clone 25908. SEQ ID NO: 344 is the determined cDNA sequence for clone 25909. SEQ ID NO: 345 is the determined cDNA sequence for clone 25910. 10 SEQ ID NO: 346 is the determined cDNA sequence for clone 25911. SEQ ID NO: 347 is the determined cDNA sequence for clone 25912. SEQ ID NO: 348 is the determined cDNA sequence for clone 25913. SEQ ID NO: 349 is the determined cDNA sequence for clone 25914. 15 SEQ ID NO: 350 is the determined cDNA sequence for clone 25915. SEQ ID NO: 351 is the determined cDNA sequence for clone 25916. SEQ ID NO: 352 is the determined cDNA sequence for clone 25917. SEQ ID NO: 353 is the determined cDNA sequence for clone 25918. SEQ ID NO: 354 is the determined cDNA sequence for clone 25919. SEQ ID NO: 355 is the determined cDNA sequence for clone 25920. 20 SEQ ID NO: 356 is the determined cDNA sequence for clone 25921. SEQ ID NO: 357 is the determined cDNA sequence for clone 25922. SEQ ID NO: 358 is the determined cDNA sequence for clone 25924. SEQ ID NO: 359 is the determined cDNA sequence for clone 25925. SEQ ID NO: 360 is the determined cDNA sequence for clone 25926. 25 SEQ ID NO: 361 is the determined cDNA sequence for clone 25927. SEQ ID NO: 362 is the determined cDNA sequence for clone 25928. SEQ ID NO: 363 is the determined cDNA sequence for clone 25929. SEQ ID NO: 364 is the determined cDNA sequence for clone 25930. SEQ ID NO: 365 is the determined cDNA sequence for clone 25931. 30 SEQ ID NO: 366 is the determined cDNA sequence for clone 25932.

SEQ ID NO: 367 is the determined cDNA sequence for clone 25933. SEQ ID NO: 368 is the determined cDNA sequence for clone 25934. SEQ ID NO: 369 is the determined cDNA sequence for clone 25935. SEQ ID NO: 370 is the determined cDNA sequence for clone 25936. 5 SEQ ID NO: 371 is the determined cDNA sequence for clone 25939. SEQ ID NO: 372 is the determined cDNA sequence for clone 32016. SEQ ID NO: 373 is the determined cDNA sequence for clone 32021. SEQ ID NO: 374 is the determined cDNA sequence for clone 31993. SEQ ID NO: 375 is the determined cDNA sequence for clone 31997. 10 SEQ ID NO: 376 is the determined cDNA sequence for clone 31942. SEQ ID NO: 377 is the determined cDNA sequence for clone 31937. SEQ ID NO: 378 is the determined cDNA sequence for clone 31952. SEQ ID NO: 379 is the determined cDNA sequence for clone 31992. SEQ ID NO: 380 is the determined cDNA sequence for clone 31961. 15 SEQ ID NO: 381 is the determined cDNA sequence for clone 31964. SEQ ID NO: 382 is the determined cDNA sequence for clone 32005. SEQ ID NO: 383 is the determined cDNA sequence for clone 31980. SEQ ID NO: 384 is the determined cDNA sequence for clone 31940. SEQ ID NO: 385 is the determined cDNA sequence for clone 32004. 20 SEQ ID NO: 386 is the determined cDNA sequence for clone 31956. SEQ ID NO: 387 is the determined cDNA sequence for clone 31934. SEQ ID NO: 388 is the determined cDNA sequence for clone 31998. SEQ ID NO: 389 is the determined cDNA sequence for clone 31973. SEQ ID NO: 390 is the determined cDNA sequence for clone 31976. 25 SEQ ID NO: 391 is the determined cDNA sequence for clone 31988. SEQ ID NO: 392 is the determined cDNA sequence for clone 31948. SEQ ID NO: 393 is the determined cDNA sequence for clone 32013. SEQ ID NO: 394 is the determined cDNA sequence for clone 31986. SEQ ID NO: 395 is the determined cDNA sequence for clone 31954. SEQ ID NO: 396 is the determined cDNA sequence for clone 31987. 30 SEQ ID NO: 397 is the determined cDNA sequence for clone 32029.

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SEQ ID NO: 398 is the determined cDNA sequence for clone 32028. SEQ ID NO: 399 is the determined cDNA sequence for clone 32012. SEQ ID NO: 400 is the determined cDNA sequence for clone 31959. SEQ ID NO: 401 is the determined cDNA sequence for clone 32027. SEQ ID NO: 402 is the determined cDNA sequence for clone 31957. SEQ ID NO: 403 is the determined cDNA sequence for clone 31950. SEQ ID NO: 404 is the determined cDNA sequence for clone 32011. SEQ ID NO: 405 is the determined cDNA sequence for clone 32022. SEQ ID NO: 406 is the determined cDNA sequence for clone 32014. SEQ ID NO: 407 is the determined cDNA sequence for clone 31963. SEQ ID NO: 408 is the determined cDNA sequence for clone 31989. SEQ ID NO: 409 is the determined cDNA sequence for clone 32015. SEQ ID NO: 410 is the determined cDNA sequence for clone 32002. SEQ ID NO: 411 is the determined cDNA sequence for clone 31939. SEQ ID NO: 412 is the determined cDNA sequence for clone 32003. SEQ ID NO: 413 is the determined cDNA sequence for clone 31936. SEQ ID NO: 414 is the determined cDNA sequence for clone 32007. SEQ ID NO: 415 is the determined cDNA sequence for clone 31965. SEQ ID NO: 416 is the determined cDNA sequence for clone 31935. SEQ ID NO: 417 is the determined cDNA sequence for clone 32008. SEQ ID NO: 418 is the determined cDNA sequence for clone 31966. SEQ ID NO: 419 is the determined cDNA sequence for clone 32020. SEQ ID NO: 420 is the determined cDNA sequence for clone 31971. SEQ ID NO: 421 is the determined cDNA sequence for clone 31977. SEQ ID NO: 422 is the determined cDNA sequence for clone 31985. SEQ ID NO: 423 is the determined cDNA sequence for clone 32023. SEQ ID NO: 424 is the determined cDNA sequence for clone 31981. SEQ ID NO: 425 is the determined cDNA sequence for clone 32006. SEQ ID NO: 426 is the determined cDNA sequence for clone 31991. SEQ ID NO: 427 is the determined cDNA sequence for clone 31995. SEQ ID NO: 428 is the determined cDNA sequence for clone 32000.

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SEQ ID NO: 429 is the determined cDNA sequence for clone 31990. SEQ ID NO: 430 is the determined cDNA sequence for clone 31946. SEQ ID NO: 431 is the determined cDNA sequence for clone 31938. SEQ ID NO: 432 is the determined cDNA sequence for clone 31941. SEQ ID NO: 433 is the determined cDNA sequence for clone 31982. 5 SEQ ID NO: 434 is the determined cDNA sequence for clone 31996. SEQ ID NO: 435 is the determined cDNA sequence for clone 32010. SEQ ID NO: 436 is the determined cDNA sequence for clone 31974. SEQ ID NO: 437 is the determined cDNA sequence for clone 31983. 10 SEQ ID NO: 438 is the determined cDNA sequence for clone 31999. SEQ ID NO: 439 is the determined cDNA sequence for clone 31949. SEQ ID NO: 440 is the determined cDNA sequence for clone 31947. SEQ ID NO: 441 is the determined cDNA sequence for clone 31994. SEQ ID NO: 442 is the determined cDNA sequence for clone 31958. SEQ ID NO: 443 is the determined cDNA sequence for clone 31975. 15 SEQ ID NO: 444 is the determined cDNA sequence for clone 31984. SEQ ID NO: 445 is the determined cDNA sequence for clone 32024. SEQ ID NO: 446 is the determined cDNA sequence for clone 31972. SEQ ID NO: 447 is the determined cDNA sequence for clone 31943. 20 SEQ ID NO: 448 is the determined cDNA sequence for clone 32018. SEQ ID NO: 449 is the determined cDNA sequence for clone 32026. SEQ ID NO: 450 is the determined cDNA sequence for clone 32009. SEQ ID NO: 451 is the determined cDNA sequence for clone 32019. SEQ ID NO: 452 is the determined cDNA sequence for clone 32025. 25 SEQ ID NO: 453 is the determined cDNA sequence for clone 31967. SEQ ID NO: 454 is the determined cDNA sequence for clone 31968. SEQ ID NO: 455 is the determined cDNA sequence for clone 31955. SEQ ID NO: 456 is the determined cDNA sequence for clone 31951. SEQ ID NO: 457 is the determined cDNA sequence for clone 31970. SEQ ID NO: 458 is the determined cDNA sequence for clone 31962. 30 SEQ ID NO: 459 is the determined cDNA sequence for clone 32001.

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SEQ ID NO: 460 is the determined cDNA sequence for clone 31953. SEQ ID NO: 461 is the determined cDNA sequence for clone 31944. SEQ ID NO: 462 is the determined cDNA sequence for clone 31825. SEQ ID NO: 463 is the determined cDNA sequence for clone 31828. SEQ ID NO: 464 is the determined cDNA sequence for clone 31830. SEQ ID NO: 465 is the determined cDNA sequence for clone 31841. SEQ ID NO: 466 is the determined cDNA sequence for clone 31847. SEQ ID NO: 467 is the determined cDNA sequence for clone 31850. SEQ ID NO: 468 is the determined cDNA sequence for clone 31852. SEQ ID NO: 469 is the determined cDNA sequence for clone 31855. SEQ ID NO: 470 is the determined cDNA sequence for clone 31858. SEQ ID NO: 471 is the determined cDNA sequence for clone 31861. SEQ ID NO: 472 is the determined cDNA sequence for clone 31868. SEQ ID NO: 473 is the determined cDNA sequence for clone 31870. SEQ ID NO: 474 is the determined cDNA sequence for clone 31872. SEQ ID NO: 475 is the determined cDNA sequence for clone 31873. SEQ ID NO: 476 is the determined cDNA sequence for clone 31877. SEQ ID NO: 477 is the determined cDNA sequence for clone 31878. SEQ ID NO: 478 is the determined cDNA sequence for clone 31885. SEQ ID NO: 479 is the determined cDNA sequence for clone 31888. SEQ ID NO: 480 is the determined cDNA sequence for clone 31890. SEQ ID NO: 481 is the determined cDNA sequence for clone 31893. SEQ ID NO: 482 is the determined cDNA sequence for clone 31898. SEQ ID NO: 483 is the determined cDNA sequence for clone 31901. SEQ ID NO: 484 is the determined cDNA sequence for clone 31909. SEQ ID NO: 485 is the determined cDNA sequence for clone 31910. SEQ ID NO: 486 is the determined cDNA sequence for clone 31914. SEQ ID NO: 487 is the determined cDNA sequence for contig 1. SEQ ID NO: 488 is the determined cDNA sequence for contig 2. SEQ ID NO: 489 is the determined cDNA sequence for contig 3. SEQ ID NO: 490 is the determined cDNA sequence for contig 4.

SEQ ID NO: 491 is the determined cDNA sequence for contig 5. SEQ ID NO: 492 is the determined cDNA sequence for contig 6. SEQ ID NO: 493 is the determined cDNA sequence for contig 7. SEQ ID NO: 494 is the determined cDNA sequence for contig 8. 5 SEQ ID NO: 495 is the determined cDNA sequence for contig 9. SEQ ID NO: 496 is the determined cDNA sequence for contig 10. SEQ ID NO: 497 is the determined cDNA sequence for contig 11 SEQ ID NO: 498 is the determined cDNA sequence for contig 12 SEQ ID NO: 499 is the determined cDNA sequence for contig 13. SEO ID NO: 500 is the determined cDNA sequence for contig 14. 10 SEQ ID NO: 501 is the determined cDNA sequence for contig 15. SEQ ID NO: 502 is the determined cDNA sequence for contig 16. SEQ ID NO: 503 is the determined cDNA sequence for contig 17. SEQ ID NO: 504 is the determined cDNA sequence for contig 18. 15 SEQ ID NO: 505 is the determined cDNA sequence for contig 19. SEQ ID NO: 506 is the determined cDNA sequence for contig 20. SEQ ID NO: 507 is the determined cDNA sequence for contig 21. SEQ ID NO: 508 is the determined cDNA sequence for contig 22. SEQ ID NO: 509 is the determined cDNA sequence for contig 23. 20 SEQ ID NO: 510 is the determined cDNA sequence for contig 24. SEQ ID NO: 511 is the determined cDNA sequence for contig 25. SEQ ID NO: 512 is the determined cDNA sequence for contig 26. SEQ ID NO: 513 is the determined cDNA sequence for contig 27. SEQ ID NO: 514 is the determined cDNA sequence for contig 28. SEQ ID NO: 515 is the determined cDNA sequence for contig 29. 25 SEQ ID NO: 516 is the determined cDNA sequence for contig 30. SEQ ID NO: 517 is the determined cDNA sequence for contig 31. SEQ ID NO: 518 is the determined cDNA sequence for contig 32. SEQ ID NO: 519 is the determined cDNA sequence for contig 33. SEQ ID NO: 520 is the determined cDNA sequence for contig 34. 30 SEQ ID NO: 521 is the determined cDNA sequence for contig 35.

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SEQ ID NO: 522 is the determined cDNA sequence for contig 36. SEQ ID NO: 523 is the determined cDNA sequence for contig 37. SEQ ID NO: 524 is the determined cDNA sequence for contig 38. SEQ ID NO: 525 is the determined cDNA sequence for contig 39. SEQ ID NO: 526 is the determined cDNA sequence for contig 40. SEQ ID NO: 527 is the determined cDNA sequence for contig 41. SEQ ID NO: 528 is the determined cDNA sequence for contig 42. SEQ ID NO: 529 is the determined cDNA sequence for contig 43. SEQ ID NO: 530 is the determined cDNA sequence for contig 44. SEQ ID NO: 531 is the determined cDNA sequence for contig 45. SEQ ID NO: 532 is the determined cDNA sequence for contig 46. SEQ ID NO: 533 is the determined cDNA sequence for contig 47. SEQ ID NO: 534 is the determined cDNA sequence for contig 48. SEQ ID NO: 535 is the determined cDNA sequence for contig 49. SEQ ID NO: 536 is the determined cDNA sequence for contig 50. SEQ ID NO: 537 is the determined cDNA sequence for contig 51. SEQ ID NO: 538 is the determined cDNA sequence for contig 52. SEQ ID NO: 539 is the determined cDNA sequence for contig 53. SEQ ID NO: 540 is the determined cDNA sequence for contig 54. SEQ ID NO: 541 is the determined cDNA sequence for contig 55. SEQ ID NO: 542 is the determined cDNA sequence for contig 56. SEQ ID NO: 543 is the determined cDNA sequence for contig 58. SEQ ID NO: 544 is the determined cDNA sequence for contig 59. SEQ ID NO: 545 is the determined cDNA sequence for contig 60. SEQ ID NO: 546 is the determined cDNA sequence for contig 61. SEQ ID NO: 547 is the determined cDNA sequence for contig 62. SEQ ID NO: 548 is the determined cDNA sequence for contig 63. SEQ ID NO: 549 is the determined cDNA sequence for contig 64. SEQ ID NO: 550 is the determined cDNA sequence for contig 65. SEQ ID NO: 551 is the determined cDNA sequence for contig 66. SEQ ID NO: 552 is the determined cDNA sequence for contig 67.

	SEQ ID NO: 553 is the determined cDNA sequence for contig 68.
•	SEQ ID NO: 554 is the determined cDNA sequence for contig 69.
	SEQ ID NO: 555 is the determined cDNA sequence for contig 70.
	SEQ ID NO: 556 is the determined cDNA sequence for contig 71.
5	SEQ ID NO: 557 is the determined cDNA sequence for contig 72.
	SEQ ID NO: 558 is the determined cDNA sequence for contig 73.
	SEQ ID NO: 559 is the determined cDNA sequence for contig 74.
	SEQ ID NO: 560 is the determined cDNA sequence for contig 75.
	SEQ ID NO: 561 is the determined cDNA sequence for contig 76.
10	SEQ ID NO: 562 is the determined cDNA sequence for contig 77.
	SEQ ID NO: 563 is the determined cDNA sequence for contig 78.
	SEQ ID NO: 564 is the determined cDNA sequence for contig 79.
	SEQ ID NO: 565 is the determined cDNA sequence for contig 80.
	SEQ ID NO: 566 is the determined cDNA sequence for contig 81.
15 .	SEQ ID NO: 567 is the determined cDNA sequence for contig 82a
	SEQ ID NO: 568 is the determined cDNA sequence for contig 83.
	SEQ ID NO: 569 is the determined cDNA sequence for clone CS1-101.
	SEQ ID NO: 570 is the determined cDNA sequence for clone CS1-102.
	SEQ ID NO: 571 is the determined cDNA sequence for clone CS1-104.
20	SEQ ID NO: 572 is the determined cDNA sequence for clone CS1-105.
	SEQ ID NO: 573 is the determined 3' cDNA sequence for clone CS1-106
	SEQ ID NO: 574 is the determined 5' cDNA sequence for clone CS1-106
	SEQ ID NO: 575 is the determined cDNA sequence for clone CS1-114.
	SEQ ID NO: 576 is the determined cDNA sequence for clone CS1-118.
25	SEQ ID NO: 577 is the determined cDNA sequence for clone CS1-120.
	SEQ ID NO: 578 is the determined cDNA sequence for clone CS1-123.
	SEQ ID NO: 579 is the determined 3' cDNA sequence for clone CS1-124
	SEQ ID NO: 580 is the determined 5' cDNA sequence for clone CS1-124
	SEQ ID NO: 581 is the determined cDNA sequence for clone CS1-128.
30	SEQ ID NO: 582 is the determined cDNA sequence for clone CS1-132.
	SEO ID NO: 583 is the determined cDNA sequence for clone CS1 136

SEQ ID NO: 584 is the determined cDNA sequence for clone CS1-137. SEQ ID NO: 585 is the determined cDNA sequence for clone CS1-139. SEQ ID NO: 586 is the determined cDNA sequence for clone CS1-141. SEQ ID NO: 587 is the determined cDNA sequence for clone CS1-152. 5 SEQ ID NO: 588 is the determined cDNA sequence for clone CS1-154. SEQ ID NO: 589 is the determined cDNA sequence for clone CS1-156. SEQ ID NO: 590 is the determined cDNA sequence for clone CS1-158. SEQ ID NO: 591 is the determined cDNA sequence for clone CS1-160. SEQ ID NO: 592 is the determined cDNA sequence for clone CS1-168. 10 SEQ ID NO: 593 is the determined cDNA sequence for clone CS1-169. SEQ ID NO: 594 is the determined cDNA sequence for clone CS1-171. SEQ ID NO: 595 is the determined cDNA sequence for clone CS1-176. SEQ ID NO: 596 is the determined cDNA sequence for clone CS1-178. SEQ ID NO: 597 is the determined cDNA sequence for clone CS1-180. 15 SEQ ID NO: 598 is the determined cDNA sequence for clone CS1-183. SEQ ID NO: 599 is the determined cDNA sequence for clone CS1-184. SEQ ID NO: 600 is the determined cDNA sequence for clone CS1-187. SEQ ID NO: 601 is the determined cDNA sequence for clone CS1-190. SEQ ID NO: 602 is the determined cDNA sequence for clone CS1-194. 20 SEQ ID NO: 603 is the determined cDNA sequence for clone CS1-195. SEQ ID NO: 604 is the determined cDNA sequence for clone CS1-196. SEQ ID NO: 605 is the determined cDNA sequence for clone CS1-197. SEQ ID NO: 606 is the determined cDNA sequence for clone CS1-200. SEQ ID NO: 607 is the determined cDNA sequence for clone CS1-206. 25 SEQ ID NO: 608 is the determined cDNA sequence for clone CS1-207. SEQ ID NO: 609 is the determined cDNA sequence for clone CS1-234. SEQ ID NO: 610 is the determined cDNA sequence for clone CS1-238. SEQ ID NO: 611 is the determined cDNA sequence for clone CS1-239. SEQ ID NO: 612 is the determined cDNA sequence for clone CS1-243. 30 SEQ ID NO: 613 is the determined cDNA sequence for clone CS1-246. SEQ ID NO: 614 is the determined cDNA sequence for clone CS1-249.

SEQ ID NO: 615 is the determined cDNA sequence for clone CS1-250. SEQ ID NO: 616 is the determined cDNA sequence for clone CS1-252. SEQ ID NO: 617 is the determined cDNA sequence for clone CT502. SEQ ID NO: 618 is the determined cDNA sequence for clone CT507. SEQ ID NO: 619 is the determined cDNA sequence for clone CT521. 5 SEQ ID NO: 620 is the determined cDNA sequence for clone CT544. SEQ ID NO: 621 is the determined cDNA sequence for clone CT577. SEQ ID NO: 622 is the determined cDNA sequence for clone CT580. SEQ ID NO: 623 is the determined cDNA sequence for clone CT594. 10 SEQ ID NO: 624 is the determined cDNA sequence for clone CT606. SEQ ID NO: 625 is the determined cDNA sequence for clone CT607. SEQ ID NO: 626 is the determined cDNA sequence for clone CT599. SEQ ID NO: 627 is the determined cDNA sequence for clone CT632. SEQ ID NO: 628 is the determined cDNA sequence for clone 35691. 15 SEQ ID NO: 629 is the determined cDNA sequence for clone 35707. SEQ ID NO: 630 is the determined cDNA sequence for clone CSE-2. SEQ ID NO: 631 is the amino acid sequence for clone CSE-2. SEQ ID NO: 632 is the determined cDNA sequence for clone CT2-1. SEQ ID NO: 633 is the determined cDNA sequence for clone CT2-6. 20 SEQ ID NO: 634 is the determined cDNA sequence for clone CT2-8. SEQ ID NO: 635 is the determined cDNA sequence for clone CT2-9. SEQ ID NO: 636 is the determined cDNA sequence for clone CT2-12. SEQ ID NO: 637 is the determined cDNA sequence for clone CT2-15. SEQ ID NO: 638 is the determined cDNA sequence for clone CT2-16. 25 SEQ ID NO: 639 is the determined cDNA sequence for clone CT2-17. SEQ ID NO: 640 is the determined cDNA sequence for clone CT2-19. SEQ ID NO: 641 is the determined cDNA sequence for clone CT2-23. SEQ ID NO: 642 is the determined cDNA sequence for clone CT2-25. SEQ ID NO: 643 is the determined cDNA sequence for clone CT2-27. 30 SEQ ID NO: 644 is the determined cDNA sequence for clone CT2-35. SEQ ID NO: 645 is the determined cDNA sequence for clone CT2-39.

SEQ ID NO: 646 is the determined cDNA sequence for clone CT2-41. SEQ ID NO: 647 is the determined cDNA sequence for clone CT2-43. SEQ ID NO: 648 is the determined cDNA sequence for clone CT2-44. SEQ ID NO: 649 is the determined cDNA sequence for clone CT2-53. SEQ ID NO: 650 is the determined cDNA sequence for clone CT2-54. 5 SEQ ID NO: 651 is the determined cDNA sequence for clone CT2-55. SEO ID NO: 652 is the determined cDNA sequence for clone CT2-57. SEQ ID NO: 653 is the determined cDNA sequence for clone CT2-60. SEQ ID NO: 654 is the determined cDNA sequence for clone CT2-64. SEQ ID NO: 655 is the determined cDNA sequence for clone CT2-67. 10 SEQ ID NO: 656 is the determined cDNA sequence for clone CT2-68. SEO ID NO: 657 is the determined cDNA sequence for clone CT2-75. SEQ ID NO: 658 is the determined cDNA sequence for clone CT2-79. SEQ ID NO: 659 is the determined cDNA sequence for clone CT2-109. SEQ ID NO: 660 is the determined cDNA sequence for clone CT2-112. 15 SEO ID NO: 661 is the determined cDNA sequence for clone CT2-127. SEQ ID NO: 662 is the determined cDNA sequence for clone CT2-129. SEO ID NO: 663 is the determined cDNA sequence for clone CT2-156. SEQ ID NO: 664 is the determined cDNA sequence for clone CT2-162. SEQ ID NO: 665 is the determined cDNA sequence for clone CT2-167. 20 SEQ ID NO: 666 is the determined cDNA sequence for clone CT2-169. SEQ ID NO: 667 is the determined cDNA sequence for clone CT2-172. SEO ID NO: 668 is the determined cDNA sequence for clone CT2-173. SEQ ID NO: 669 is the determined cDNA sequence for clone CT2-174. SEO ID NO: 670 is the determined cDNA sequence for clone CT2-177. 25 SEQ ID NO: 671 is the determined cDNA sequence for clone CT2-181. SEO ID NO: 672 is the determined cDNA sequence for clone CT2-191. SEQ ID NO: 673 is the determined cDNA sequence for clone CT2-192. SEQ ID NO: 674 is the determined cDNA sequence for clone CT2-207. SEQ ID NO: 675 is the determined cDNA sequence for clone CT2-222. 30 SEQ ID NO: 676 is the determined cDNA sequence for clone CT2-223. 5

15

SEQ ID NO: 677 is the determined cDNA sequence for clone CT2-233.

SEQ ID NO: 678 is the determined cDNA sequence for clone CT2-244.

SEQ ID NO: 679 is the determined cDNA sequence for clone CT2-257.

SEQ ID NO: 680 is the determined cDNA sequence for clone CT2-279.

SEQ ID NO: 681 is the determined cDNA sequence for clone CT2-288.

SEQ ID NO: 682 is the determined cDNA sequence for clone CT2-291.

SEQ ID NO:683 is the full-length cDNA sequence for human PAC (SEQ ID NOs: 18 and 19).

SEQ ID NO:684 is the full-length cDNA sequence for murine homologue of human PAC (SEQ ID NO: 683).

SEQ ID NO:685 is the predicted amino acid sequence for the clone of SEQ ID NO:683.

SEQ ID NO:686 is a longer determined cDNA sequence for clone CoSub-19 (SEQ ID NO:138).

SEQ ID NO:687 is the predicted amino acid sequence for the clone of SEQ ID NO:686.

SEQ ID NO:688 is the nucleotide sequence of the M13 forward primer.

SEQ ID NO:689 is the nucleotide sequence of the M13 reverse primer.

SEQ ID NO:690 is a longer determined cDNA sequence for C799P (SEQ ID NO:40), showing homology to homo sapiens NADH/NADPH thyroid oxidase p138-tox mRNA.

SEQ ID NO:691 is a longer determined cDNA sequence for C794P (SEQ ID NO:41).

SEQ ID NO:692 is the predicted amino acid sequence for the clone of SEQ ID NO:690.

SEQ ID NO:693 is the predicted amino acid sequence for the clone of SEQ ID NO:691.

SEQ ID NO: 694 is the determined cDNA sequence for clone R0093:A03.

30 SEQ ID NO: 695 is the determined cDNA sequence for clone R0093:A10.

SEQ ID NO: 696 is the determined cDNA sequence for clone R0093:A11. SEQ ID NO: 697 is the determined cDNA sequence for clone R0093:A12. SEQ ID NO: 698 is the determined cDNA sequence for clone R0093:B03. SEQ ID NO: 699 is the determined cDNA sequence for clone R0093:B04. SEQ ID NO: 700 is the determined cDNA sequence for clone R0093:B09. 10 SEQ ID NO: 701 is the determined cDNA sequence for clone R0093:B10. SEQ ID NO: 702 is the determined cDNA sequence for clone R0093:B11. SEQ ID NO: 703 is the determined cDNA sequence for clone 15 R0093:B12. SEQ ID NO: 704 is the determined cDNA sequence for clone R0093:C01. SEQ ID NO: 705 is the determined cDNA sequence for clone R0093:C03. 20 SEQ ID NO: 706 is the determined cDNA sequence for clone R0093:C04. SEQ ID NO: 707 is the determined cDNA sequence for clone R0093:C06. SEQ ID NO: 708 is the determined cDNA sequence for clone 25 R0093:C08. SEQ ID NO: 709 is the determined cDNA sequence for clone R0093:C09. SEQ ID NO: 710 is the determined cDNA sequence for clone R0093:C10. 30 SEQ ID NO: 711 is the determined cDNA sequence for clone

R0093:C11. SEO ID NO: 712 is the determined cDNA sequence for clone R0093:C12. SEO ID NO: 713 is the determined cDNA sequence for clone R0093:D01. SEQ ID NO: 714 is the determined cDNA sequence for clone R0093:D02. SEO ID NO: 715 is the determined cDNA sequence for clone R0093:D03. SEO ID NO: 716 is the determined cDNA sequence for clone 10 R0093:D04. SEQ ID NO: 717 is the determined cDNA sequence for clone R0093:D05. SEO ID NO: 718 is the determined cDNA sequence for clone R0093:D06. SEQ ID NO: 719 is the determined cDNA sequence for clone R0093:D07. SEQ ID NO: 720 is the determined cDNA sequence for clone R0093:D08. SEQ ID NO: 721 is the determined cDNA sequence for clone 20 R0093:D10. SEQ ID NO: 722 is the determined cDNA sequence for clone R0093:D11. SEQ ID NO: 723 is the determined cDNA sequence for clone R0093:E02. SEQ ID NO: 724 is the determined cDNA sequence for clone R0093:E03. SEQ ID NO: 725 is the determined cDNA sequence for clone R0093:E04. SEQ ID NO: 726 is the determined cDNA sequence for clone 30 R0093:E06.

		SEQ	ID	NO:	727	is	the	determined	cDNA	sequence	for	clone
	R0093:E07.	٠										
		SEQ	ID	NO:	728	is	the	determined	cDNA	sequence	for	clone
_	R0093:E08.	aro	ID	110	700				722.4		^	
5	R0093:E09.	SEQ	ענ	NO:	729	15	the	determined	cDNA	sequence	ior	cione
	10075.E07.	SEQ	ID	NO:	730	is	the	determined	cDNA	sequence	for	clone
	R0093:E10.									•		
		SEQ	ID	NO:	731	is	the	determined	cDNA	sequence	for	clone
10	R0093:E11.											
	D0002-E02	SEQ	ID	NO:	732	is	the	determined	cDNA	sequence	for	clone
	R0093:F02.	SEO	ID	NO:	733	is	the	determined	cDNA	sequence	for	clone
	R0093:F03.	~~~		2.0.	.55	10		401011111100		podanio	101	0.0
15		SEQ	ID	NO:	734	is	the	determined	cDNA	sequence	for	clone
	R0093:F04.											
	D0002-E05	SEQ	ID	NO:	735	is	the	determined	cDNA	sequence	for	clone
	R0093:F05.	SEO	מו	NO.	736	is	the	determined	cDNA	seguence	for	clone
20	R0093:F06.	224	110	11,01	150	10	uio	dotommed	ODIVII	soquoneo	101	Ciono
	•	SEQ	ID	NO:	737	is	the	determined	cDNA	sequence	for	clone
	R0093:F08.											
		SEQ	ID	NO:	738	is	the	determined	cDNA	sequence	for	clone
25	R0093:F09.	SEO.	ID	NO.	720	i.	414.0	datamainad	aDNI A		for	alama
25	R0093:F10.	DEQ		NO.	137	12	une	determined	CDNA	sequence	101	Cione
		SEQ	\mathbf{m}	NO:	740	is	the	determined	cDNA	sequence	for	clone
	R0093:F12.											
		SEQ	ID	'nΟ:	741	is	the	determined	cDNA	sequence	for	clone
30	R0093:G01.	an ^	**	220				•	-		•	
		SEQ	ID	NO:	742	is	the	determined	cDNA	sequence	tor	clone

R0093:G03. SEO ID NO: 743 is the determined cDNA sequence for clone R0093:G04. SEQ ID NO: 744 is the determined cDNA sequence for clone R0093:G06. SEQ ID NO: 745 is the determined cDNA sequence for clone R0093:G07. SEQ ID NO: 746 is the determined cDNA sequence for clone R0093:G08. SEQ ID NO: 747 is the determined cDNA sequence for clone 10 R0093:G09. SEQ ID NO: 748 is the determined cDNA sequence for clone R0093:G10. SEQ ID NO: 749 is the determined cDNA sequence for clone R0093:G11. SEQ ID NO: 750 is the determined cDNA sequence for clone R0093:G12. SEQ ID NO: 751 is the determined cDNA sequence for clone R0093:H02. SEQ ID NO: 752 is the determined cDNA sequence for clone 20 R0093:H03. SEQ ID NO: 753 is the determined cDNA sequence for clone R0093:H04. SEQ ID NO: 754 is the determined cDNA sequence for clone R0093:H05. 25 SEQ ID NO: 755 is the determined cDNA sequence for clone R0093:H07. SEQ ID NO: 756 is the determined cDNA sequence for clone R0093:H08. SEQ ID NO: 757 is the determined cDNA sequence for clone 30 R0093:H09.

	D0000 TV40	SEQ	ID	NO:	758	is	the	determined	cDNA	sequence	for	clone
	R0093:H10.	SEQ	ID	NO:	759	is	the	determined	cDNA	sequence	for	clone
	R0093:H11.											
5	R0094:A03.	SEQ	ID	NO:	760	is	the	determined	cDNA	sequence	for	clone
	1,000 1,112021	SEQ	ID	NO:	761	is	the	determined	cDNA	sequence	for	clone
	R0094:A05.	SEO	מז	NO.	762	is	the	determined	cDNA	sequence	for	clone
10	R0094:A06.	DLQ	110	110.		45	1110		V 21111	50400000		
	R0094:A07.	SEQ	ID	NO:	763	is	the	. determined	cDNA	sequence	for	clone
	K0094.A07.	SEQ	ID	NO:	764	is	the	determined	cDNA	sequence	for	clone
1.5	R0094:A09.	GE()	ĭŊ	N/Ω.	765	in	tha	determined	cDNA	Seguence	for	clone
15	R0094:A10.	SEQ	ענג	NO.	703	15	uic	determined	CDINA	sequence	101	CIOIIC
	D0004-A12	SEQ	ID	NO:	766	is	the	determined	cDNA	sequence	for	clone
	R0094:A12.	SEQ	ID	NO:	767	is	the	determined	cDNA	sequence	for	clone
20	R0094:B03.	CEO		'NIO.	. 760	:-	4lan	dotomoinod	aTNI A	goguanoa	for	alone
	R0094:B06.	SEQ	ענ	NO:	/08	18	uie	determined	CDINA	sequence	101	CIOHE
	D0004 D00	SEQ	ID	NO:	769	is	the	determined	cDNA	sequence	for	clone
25	R0094:B08.	SEQ	ID	NO:	770	is	the	determined	cDNA	sequence	for	clone
	R0094:B11.		•••						77.7.1		c	•
	R0094:B12.	SEQ	, ID	NO:	771	15	the	determined	cDNA	sequence	ior	cione
		SEQ	ID	NO:	772	is	the	determined	cDNA	sequence	for	clone
30	R0094:C01.	SEQ	ID	NO:	773	is	the	determined	cDNA	sequence	for	clone

R0094:C02. SEQ ID NO: 774 is the determined cDNA sequence for clone R0094:C03. SEQ ID NO: 775 is the determined cDNA sequence for clone R0094:C05. SEQ ID NO: 776 is the determined cDNA sequence for clone R0094:C06. SEQ ID NO: 777 is the determined cDNA sequence for clone R0094:C08. SEQ ID NO: 778 is the determined cDNA sequence for clone 10 R0094:C09. SEQ ID NO: 779 is the determined cDNA sequence for clone R0094:C10. SEO ID NO: 780 is the determined cDNA sequence for clone R0094:C11. 15 SEQ ID NO: 781 is the determined cDNA sequence for clone R0094:C12. SEO ID NO: 782 is the determined cDNA sequence for clone R0094:D01. SEQ ID NO: 783 is the determined cDNA sequence for clone 20 R0094:D02. SEQ ID NO: 784 is the determined cDNA sequence for clone R0094:D03. SEQ ID NO: 785 is the determined cDNA sequence for clone R0094:D04. SEQ ID NO: 786 is the determined cDNA sequence for clone R0094:D05. SEQ ID NO: 787 is the determined cDNA sequence for clone R0094:D07. SEQ ID NO: 788 is the determined cDNA sequence for clone 30 R0094:D08.

SEO ID NO: 789 is the determined cDNA sequence for clone R0094:D09. SEQ ID NO: 790 is the determined cDNA sequence for clone R0094:D10. SEQ ID NO: 791 is the determined cDNA sequence for clone R0094:D12. SEO ID NO: 792 is the determined cDNA sequence for clone R0094:E01. SEQ ID NO: 793 is the determined cDNA sequence for clone R0094:E02. SEQ ID NO: 794 is the determined cDNA sequence for clone R0094:E03. SEQ ID NO: 795 is the determined cDNA sequence for clone R0094:E05. SEQ ID NO: 796 is the determined cDNA sequence for clone 15 R0094:E06. SEQ ID NO: 797 is the determined cDNA sequence for clone R0094:E07. SEQ ID NO: 798 is the determined cDNA sequence for clone R0094:E08. 20 SEQ ID NO: 799 is the determined cDNA sequence for clone R0094:E09. SEQ ID NO: 800 is the determined cDNA sequence for clone R0094:E10. SEQ ID NO: 801 is the determined cDNA sequence for clone 25 R0094:E11. SEQ ID NO: 802 is the determined cDNA sequence for clone R0094:E12. SEQ ID NO: 803 is the determined cDNA sequence for clone R0094:F01. 30 SEQ ID NO: 804 is the determined cDNA sequence for clone

R0094:F03. SEQ ID NO: 805 is the determined cDNA sequence for clone R0094:F05. SEQ ID NO: 806 is the determined cDNA sequence for clone R0094:F06. SEO ID NO: 807 is the determined cDNA sequence for clone R0094:F07. SEQ ID NO: 808 is the determined cDNA sequence for clone R0094:F08. SEQ ID NO: 809 is the determined cDNA sequence for clone 10 R0094:F09. SEO ID NO: 810 is the determined cDNA sequence for clone R0094:F10. SEQ ID NO: 811 is the determined cDNA sequence for clone R0094:F11. SEQ ID NO: 812 is the determined cDNA sequence for clone R0094:F12. SEO ID NO: 813 is the determined cDNA sequence for clone R0094:G02. SEQ ID NO: 814 is the determined cDNA sequence for clone 20 R0094:G03. SEQ ID NO: 815 is the determined cDNA sequence for clone R0094:G04. SEQ ID NO: 816 is the determined cDNA sequence for clone R0094:G06. SEQ ID NO: 817 is the determined cDNA sequence for clone R0094:G07. SEQ ID NO: 818 is the determined cDNA sequence for clone R0094:G08. SEQ ID NO: 819 is the determined cDNA sequence for clone 30 R0094:G10.

SEQ ID NO: 820 is the determined cDNA sequence for clone R0094:G11. SEQ ID NO: 821 is the determined cDNA sequence for clone R0094:G12. SEQ ID NO: 822 is the determined cDNA sequence for clone 5 R0094:H01. SEQ ID NO: 823 is the determined cDNA sequence for clone R0094:H03. SEQ ID NO: 824 is the determined cDNA sequence for clone R0094:H04. 10 SEQ ID NO: 825 is the determined cDNA sequence for clone R0094:H05. SEQ ID NO: 826 is the determined cDNA sequence for clone R0094:H06. SEQ ID NO: 827 is the determined cDNA sequence for clone 15 R0094:H08. SEQ ID NO: 828 is the determined cDNA sequence for clone R0094:H09. SEQ ID NO: 829 is the determined cDNA sequence for clone R0094:H10. 20 SEQ ID NO: 830 is the determined cDNA sequence for clone R0094:H11. SEQ ID NO: 831 is the determined cDNA sequence for clone R0095:A03. SEQ ID NO: 832 is the determined cDNA sequence for clone 25 R0095:A06. SEQ ID NO: 833 is the determined cDNA sequence for clone R0095:A07. SEQ ID NO: 834 is the determined cDNA sequence for clone R0095:B01. SEQ ID NO: 835 is the determined cDNA sequence for clone

R0095:B02. SEQ ID NO: 836 is the determined cDNA sequence for clone R0095:B03. SEQ ID NO: 837 is the determined cDNA sequence for clone R0095:B04. SEQ ID NO: 838 is the determined cDNA sequence for clone R0095:B05. SEQ ID NO: 839 is the determined cDNA sequence for clone R0095:B06. SEQ ID NO: 840 is the determined cDNA sequence for clone 10 R0095:B10. SEQ ID NO: 841 is the determined cDNA sequence for clone R0095:B11. SEQ ID NO: 842 is the determined cDNA sequence for clone R0095:B12. SEQ ID NO: 843 is the determined cDNA sequence for clone R0095:C01. SEQ ID NO: 844 is the determined cDNA sequence for clone R0095:C03. SEQ ID NO: 845 is the determined cDNA sequence for clone 20 R0095:C04. SEQ ID NO: 846 is the determined cDNA sequence for clone R0095:C05. SEQ ID NO: 847 is the determined cDNA sequence for clone R0095:C06. SEQ ID NO: 848 is the determined cDNA sequence for clone R0095:C07. SEQ ID NO: 849 is the determined cDNA sequence for clone R0095:C08. SEQ ID NO: 850 is the determined cDNA sequence for clone R0095:C10.

SEQ ID NO: 851 is the determined cDNA sequence for clone R0095:C12. SEQ ID NO: 852 is the determined cDNA sequence for clone R0095:D01. SEQ ID NO: 853 is the determined cDNA sequence for clone R0095:D03. SEQ ID NO: 854 is the determined cDNA sequence for clone R0095:D04. SEQ ID NO: 855 is the determined cDNA sequence for clone R0095:D06. 10 SEQ ID NO: 856 is the determined cDNA sequence for clone R0095:D07. SEQ ID NO: 857 is the determined cDNA sequence for clone R0095:D08. SEQ ID NO: 858 is the determined cDNA sequence for clone 15 R0095:D09. SEQ ID NO: 859 is the determined cDNA sequence for clone R0095:D11. SEQ ID NO: 860 is the determined cDNA sequence for clone R0095:D12. 20 SEQ ID NO: 861 is the determined cDNA sequence for clone R0095:E01. SEQ ID NO: 862 is the determined cDNA sequence for clone R0095:E02. 25 SEQ ID NO: 863 is the determined cDNA sequence for clone R0095:E04. SEQ ID NO: 864 is the determined cDNA sequence for clone R0095:E05. SEQ ID NO: 865 is the determined cDNA sequence for clone R0095:E06. 30 SEQ ID NO: 866 is the determined cDNA sequence for clone

		R0095:E07.											
		D0005-T00	SEQ	ID	NO:	867	is	the	determined	cDNA	sequence	for	clone
		R0095:E08.	SEQ	ID	NO:	868	is	the	determined	cDNA	sequence	for	clone
	5	R0095:E11.	CE()	TD.	NO.	960	:-	4ha	dataminad	aDM A	g0g110m00	for-	alona
		R0095:E12.	SEQ	טנ	NO:	809	18	uie	determined	CDNA	sequence	101	Cione
		D0005-F01	SEQ	ID	NO:	870	is	the	determined	cDNA	sequence	for	clone
	10	R0095:F01.	SEQ	ID	NO:	871	is	the	determined	cDNA	sequence	for	clone
•		R0095:F03.	aro.	TD.	NO.	072	•_	41	4.4	~DNIA		£	alama
		R0095:F06.	SEQ	עו	NO:	8/2	15	tne	determined	CDNA	sequence	ior	cione
	1.5	D0005-E10	SEQ	ID	NO:	873	is	the	determined	cDNA	sequence	for	clone
	15	R0095:F10.	SEQ	ID	NO:	874	is	the	determined	cDNA	sequence	for	clone
		R0095:F11.	SEO	ID	NO.	975	.	the	determined	cDNA	caduanca	for	clone
		R0095:G02.	SEQ	ענ	NO.	0/3	19	ше	determined	CDNA	sequence	101	Clone
	20	R0095:G03.	SEQ	ID	NO:	876	is	the	determined	cDNA	sequence	for	clone
		K0093.G03.	SEQ	ID	NO:	877	is	the	determined	cDNA	sequence	for	clone
		R0095:G04.	CEO	m	NO.	070	:-	+ha	determined	•DMA	ooguanga.	for	alana
	25	R0095:G08.	yac	ID	NO.	0/0	12	ше	determined	CDNA	sequence	101	Cione
		R0095:G09.	SEQ	ID	NO:	879	is	the	determined	cDNA	sequence	for	clone
		K0095:G09.	SEQ	ID	NO:	880	is	the	determined	cDNA	sequence	for	clone
	20	R0095:G10.	SEV.	עו	N ∩ •	Q01	:.	tha	determined	¢DNI ≬	pegnence	for	olona
	30	R0095:H01.	оцŲ	ענג	110.	001	12	u16	determined	ODIVA	soquence	101	CIOHE

SEQ ID NO: 882 is the determined cDNA sequence for clone R0095:H02. SEQ ID NO: 883 is the determined cDNA sequence for clone R0095:H04. SEQ ID NO: 884 is the determined cDNA sequence for clone R0095:H06. SEQ ID NO: 885 is the determined cDNA sequence for clone R0095:H07. SEQ ID NO: 886 is the determined cDNA sequence for clone R0095:H09. SEQ ID NO: 887 is the determined cDNA sequence for clone R0096:A02. SEQ ID NO: 888 is the determined cDNA sequence for clone R0096:A08. SEQ ID NO: 889 is the determined cDNA sequence for clone 15 R0096:A09. SEQ ID NO: 890 is the determined cDNA sequence for clone R0096:A10. SEQ ID NO: 891 is the determined cDNA sequence for clone R0096:A11. SEQ ID NO: 892 is the determined cDNA sequence for clone R0096:A12. SEQ ID NO: 893 is the determined cDNA sequence for clone R0096:B02. SEQ ID NO: 894 is the determined cDNA sequence for clone 25 R0096:B03. SEQ ID NO: 895 is the determined cDNA sequence for clone R0096:B04. SEQ ID NO: 896 is the determined cDNA sequence for clone R0096:B05. SEQ ID NO: 897 is the determined cDNA sequence for clone

R0096:B06. SEQ ID NO: 898 is the determined cDNA sequence for clone R0096:B07. SEQ ID NO: 899 is the determined cDNA sequence for clone R0096:B08. SEO ID NO: 900 is the determined cDNA sequence for clone R0096:B09. SEO ID NO: 901 is the determined cDNA sequence for clone R0096:B10. SEQ ID NO: 902 is the determined cDNA sequence for clone 10 R0096:B11. SEQ ID NO: 903 is the determined cDNA sequence for clone R0096:B12. SEO ID NO: 904 is the determined cDNA sequence for clone R0096:C01. SEO ID NO: 905 is the determined cDNA sequence for clone R0096:C03. SEO ID NO: 906 is the determined cDNA sequence for clone R0096:C04. SEQ ID NO: 907 is the determined cDNA sequence for clone 20 R0096:C05. SEQ ID NO: 908 is the determined cDNA sequence for clone R0096:C06. SEQ ID NO: 909 is the determined cDNA sequence for clone R0096:C07. SEQ ID NO: 910 is the determined cDNA sequence for clone R0096:C08. SEQ ID NO: 911 is the determined cDNA sequence for clone R0096:C09. SEQ ID NO: 912 is the determined cDNA sequence for clone R0096:C10.

		SEQ	ID	NO:	913	is	the	determined	cDNA	sequence	for	clone
	R0096:C11.	SEO	Œ	NO·	914	ic	the	determined	cDNA	seguence	for	clone
	R0096:C12.	DDQ	ıD	110.	717	13	uic	determined	· ·	sequence	101	CIOILC
5		SEQ	ID	NO:	915	is	the	determined	cDNA	sequence	for	clone
	R0096:D01.	270	**					• • •	,			_
	R0096:D02.	SEQ	Ю	NO:	916	is	the	determined	cDNA	sequence	for	clone
		SEQ	ID	NO:	917	is	the	determined	cDNA	sequence	for	clone
10	R0096:D03.											
	R0096:D04.	SEQ	ID	NO:	918	is	the	determined	cDNA	sequence	for	. clone
	R0090.D04.	SEQ	ID	NO:	919	is	the	determined	cDNA	sequence	for	clone
	R0096:D05.											
15	R0096:D08.	SEQ	ID	NO:	920	is	the	determined	cDNA	sequence	for	clone
	K0090.D08.	SEQ	ID	NO:	921	is	the	determined	cDNA	sequence	for	clone
	R0096:D09.									•		
	D0004 D10	SEQ	ID	NO:	922	is	the	determined	cDNA	sequence	for	clone
20	R0096:D10.	SEO	ID	NO:	923	is	the	determined	cDNA	sequence	for	clone
	R0096:D12.	`										
		SEQ	ID	NO:	924	is	the	determined	cDNA	sequence	for	clone
25	R0096:E01.	SEO	m	NO.	925	is	the	determined	cDNA	segmence	for	clone
23	R0096:E02.	SEQ	110	110.	723	15	the	determined	CDIVI	sequence		CIOILC
		SEQ	ID	NO:	926	is	the	determined	cDNA	sequence	for	clone
	R0096:E03.	SEO.	עו	NO.	027	:-	41		aDNI 4	3.5.1.	c .	.1.
30	R0096:E04.	sey	IV.	110:	921	15	me	determined	CDNA	sequence	ior	cione
		SEQ	ID	NO:	928	is	the	determined	cDNA	sequence	for	clone

R0096:E05. SEQ ID NO: 929 is the determined cDNA sequence for clone R0096:E06. SEQ ID NO: 930 is the determined cDNA sequence for clone R0096:E08. SEQ ID NO: 931 is the determined cDNA sequence for clone R0096:E09. SEQ ID NO: 932 is the determined cDNA sequence for clone R0096:E10. SEO ID NO: 933 is the determined cDNA sequence for clone 10 R0096:E11. SEQ ID NO: 934 is the determined cDNA sequence for clone R0096:E12. SEQ ID NO: 935 is the determined cDNA sequence for clone R0096:F01. SEQ ID NO: 936 is the determined cDNA sequence for clone R0096:F02. SEQ ID NO: 937 is the determined cDNA sequence for clone R0096:F03. SEQ ID NO: 938 is the determined cDNA sequence for clone 20 R0096:F04. SEQ ID NO: 939 is the determined cDNA sequence for clone R0096:F05. SEQ ID NO: 940 is the determined cDNA sequence for clone R0096:F07. SEQ ID NO: 941 is the determined cDNA sequence for clone R0096:F10. SEQ ID NO: 942 is the determined cDNA sequence for clone R0096:F11. SEQ ID NO: 943 is the determined cDNA sequence for clone R0096:G01.

SEQ ID NO: 944 is the determined cDNA sequence for clone R0096:G03. SEQ ID NO: 945 is the determined cDNA sequence for clone R0096:G04. SEQ ID NO: 946 is the determined cDNA sequence for clone R0096:G05. SEQ ID NO: 947 is the determined cDNA sequence for clone R0096:G06. SEQ ID NO: 948 is the determined cDNA sequence for clone R0096:G07. SEQ ID NO: 949 is the determined cDNA sequence for clone R0096:G09. SEQ ID NO: 950 is the determined cDNA sequence for clone R0096:G10. SEQ ID NO: 951 is the determined cDNA sequence for clone 15 R0096:G12. SEQ ID NO: 952 is the determined cDNA sequence for clone R0096:H01. SEQ ID NO: 953 is the determined cDNA sequence for clone R0096:H02. 20 SEQ ID NO: 954 is the determined cDNA sequence for clone R0096:H03. SEQ ID NO: 955 is the determined cDNA sequence for clone R0096:H07. SEQ ID NO: 956 is the determined cDNA sequence for clone 25 R0096:H08. SEQ ID NO: 957 is the determined cDNA sequence for clone R0097:A05. SEQ ID NO: 958 is the determined cDNA sequence for clone R0097:A06. SEQ ID NO: 959 is the determined cDNA sequence for clone

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R0097:A10. SEQ ID NO: 960 is the determined cDNA sequence for clone R0097:A11. SEQ ID NO: 961 is the determined cDNA sequence for clone R0097:B01. SEQ ID NO: 962 is the determined cDNA sequence for clone R0097:B03. SEQ ID NO: 963 is the determined cDNA sequence for clone R0097:B04. SEQ ID NO: 964 is the determined cDNA sequence for clone 10 R0097:B05. SEQ ID NO: 965 is the determined cDNA sequence for clone R0097:B06. SEQ ID NO: 966 is the determined cDNA sequence for clone R0097:B07. SEQ ID NO: 967 is the determined cDNA sequence for clone R0097:B11. SEQ ID NO: 968 is the determined cDNA sequence for clone R0097:C01. SEQ ID NO: 969 is the determined cDNA sequence for clone 20 R0097:C02. SEQ ID NO: 970 is the determined cDNA sequence for clone R0097:C03. SEQ ID NO: 971 is the determined cDNA sequence for clone R0097:C04. SEQ ID NO: 972 is the determined cDNA sequence for clone R0097:C05. SEQ ID NO: 973 is the determined cDNA sequence for clone. R0097:C07. SEQ ID NO: 974 is the determined cDNA sequence for clone R0097:C08.

SEQ ID NO: 975 is the determined cDNA sequence for clone R0097:C09. SEQ ID NO: 976 is the determined cDNA sequence for clone R0097:C10. SEQ ID NO: 977 is the determined cDNA sequence for clone R0097:D01. SEQ ID NO: 978 is the determined cDNA sequence for clone R0097:D08. SEQ ID NO: 979 is the determined cDNA sequence for clone R0097:E02. SEQ ID NO: 980 is the determined cDNA sequence for clone R0097:E09. SEQ ID NO: 981 is the determined cDNA sequence for clone R0097:E11. SEQ ID NO: 982 is the determined cDNA sequence for clone 15 R0097:F01. SEQ ID NO: 983 is the determined cDNA sequence for clone R0097:F11. SEQ ID NO: 984 is the determined cDNA sequence for clone R0097:G01. SEQ ID NO: 985 is the determined cDNA sequence for clone R0097:G11. SEQ ID NO: 986 is the determined cDNA sequence for clone R0097:G12. SEQ ID NO: 987 is the determined cDNA sequence for clone 25 R0097:H01. SEQ ID NO: 988 is the determined cDNA sequence for clone R0097:H02. SEQ ID NO: 989 is the determined cDNA sequence for clone R0097:H04. SEQ ID NO: 990 is the determined cDNA sequence for clone

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R0097:H06. SEQ ID NO: 991 is the determined cDNA sequence for clone R0097:H07. SEQ ID NO: 992 is the determined cDNA sequence for clone R0097:H09. SEQ ID NO: 993 is the determined cDNA sequence for clone R0097:H11. SEQ ID NO: 994 is the determined cDNA sequence for clone R0098:A03. SEQ ID NO: 995 is the determined cDNA sequence for clone 10 R0098:A05. SEQ ID NO: 996 is the determined cDNA sequence for clone R0098:A06. SEQ ID NO: 997 is the determined cDNA sequence for clone R0098:A10. SEO ID NO: 998 is the determined cDNA sequence for clone R0098:A12. SEO ID NO: 999 is the determined cDNA sequence for clone R0098:B01. SEQ ID NO: 1000 is the determined cDNA sequence for clone 20 R0098:B02. SEQ ID NO: 1001 is the determined cDNA sequence for clone R0098:B05. SEQ ID NO: 1002 is the determined cDNA sequence for clone R0098:B06. SEQ ID NO: 1003 is the determined cDNA sequence for clone R0098:B10. SEQ ID NO: 1004 is the determined cDNA sequence for clone R0098:C03. SEQ ID NO: 1005 is the determined cDNA sequence for clone R0098:C04.

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SEQ ID NO: 1006 is the determined cDNA sequence for clone R0098:C05. SEQ ID NO: 1007 is the determined cDNA sequence for clone R0098:C10. SEQ ID NO: 1008 is the determined cDNA sequence for clone R0098:C11. SEQ ID NO: 1009 is the determined cDNA sequence for clone R0098:D01. SEQ ID NO: 1010 is the determined cDNA sequence for clone R0098:D02. 10 SEQ ID NO: 1011 is the determined cDNA sequence for clone R0098:D07. SEQ ID NO: 1012 is the determined cDNA sequence for clone R0098:D08. SEQ ID NO: 1013 is the determined cDNA sequence for clone 15 R0098:D09. SEQ ID NO: 1014 is the determined cDNA sequence for clone R0098:D10. SEQ ID NO: 1015 is the determined cDNA sequence for clone R0098:D11. 20 SEQ ID NO: 1016 is the determined cDNA sequence for clone R0098:D12. SEQ ID NO: 1017 is the determined cDNA sequence for clone R0098:E01. 25 SEQ ID NO: 1018 is the determined cDNA sequence for clone R0098:E04. SEQ ID NO: 1019 is the determined cDNA sequence for clone R0098:E05. SEQ ID NO: 1020 is the determined cDNA sequence for clone R0098:E06. 30 SEQ ID NO: 1021 is the determined cDNA sequence for clone

	R0098:E07.											
		SEQ	ID	NO:	1022	is	the	determined	cDNA	sequence	for	clone
	R0098:E11.	SEO	ID	NO:	1023	is	the	determined	cDNA	sequence	for	clone
5	R0098:F04.									1		
	D0000 F05	SEQ	ID	NO:	1024	is	the	determined	cDNA	sequence	for	clone
	R0098:F05.	SEQ	ID	NO:	1025	is	the	determined	cDNA	sequence	for	clone
	R0098:F06.									•		
10	R0098:F07.	SEQ	ID	NO:	1026	is	the	determined	cDNA	sequence	for	clone
	K0098.P07.	SEQ	ID	NO:	1027	is	the	determined	cDNA	sequence	for	clone
	R0098:F08.											
15	R0098:F09.	SEQ	ID	NO:	1028	is	the	determined	cDNA	sequence	for	clone
		SEQ	ID	NO:	1029	is	the	determined	cDNA	sequence	for	clone
	R0098:F10.	SEC.	ID.	NO.	1020	:_	41		-DNIA		C	_1
	R0098:F11.	SEQ	שו	NO:	1030	IS	me	determined	CDNA	sequence	ior	cione
20		SEQ	ID	NO:	1031	is	the	determined	cDNA	sequence	for	clone
	R0098:F12.	SEO	מו	NO.	1032	ic	the	determined	cDNA	Paguanca	for	clone
	R0098:G02.	DEQ	ענ	110.	1032	13	ЩС	determined	CDIVA	sequence	101	Cione
		SEQ	ID	NO:	1033	is	the	determined	cDNA	sequence	for	clone
25	R0098:G03.	SEO	ID	NO:	1034	is	the	determined	cDNA	sequence	for	clone
	R0098:G05.									1		
	70008 606	SEQ	ID	NO:	1035	is	the	determined	cDNA	sequence	for	clone
30	R0098:G06.	SEQ	ID	NO:	1036	is	the	determined	cDNA	sequence	for	clone
	R0098:G07.									-		

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	R0098:G08.	SEQ	ID	NO:	1037	İS	the	determined	cDNA	sequence	tor	clone
	R0070.G00.	SEQ	ID	NO:	1038	is	the	determined	cDNA	sequence	for	clone
	R0098:G09.											
5	R0098:G10.	SEQ	ID	NO:	1039	is	the	determined	cDNA	sequence	for	clone
	10070.010.	SEQ	ID	NO:	1040	is	the	determined	cDNA	sequence	for	clone
	R0098:G11.										_	
10	R0098:G12.	SEQ	ID	NO:	1041	is	the	determined	cDNA	sequence	for	clone
	1.0070.012.	SEQ	ID	NO:	1042	is	the	determined	cDNA	sequence	for	clone
	R0098:H02.		•						~~~			_
	R0098:H03.	SEQ	ID	NO:	1043	15	the	determined	cDNA	sequence	ior	clone
15		SEQ	ID	NO:	1044	is	the	determined	cDNA	sequence	for	clone
	R0098:H04.	gr()	ID	NO.	1045	:-	tha	datamainad	oDM A	g00110m00	fo	alama
	R0098:H05.	SEQ	ענג	NO.	1043	15	ше	determined	UDINA	sequence	101	Cione
		SEQ	ID	NO:	1046	is	the	determined	cDNA	sequence	for	clone
20	R0098:H07.	SEU.	m	NO.	1047	:.	tha	determined	oDNI A	COGUANCA	for	olone
	R0098:H08.	SEQ	ענ	NO.	1047	12	ше	determined	CDINA	sequence	101	Cione
		SEQ	ID	NO:	1048	is	the	determined	cDNA	sequence	for	clone
25	R0098:H11.	SEO	נ כוז	NIO: 1	040 ia	th:	dot	ermined cDN	IA segui	ence for al	one (~070D
25 ·	which chave	_							-			
	which shows NT2RP40019	, "			_			-				
	111210170017	o and	• 1101	aro saj	,1C112 C	יועני	•A 1'		CIUIIC I			

SEQ ID NO: 1050 is the determined cDNA sequence for clone C882P which shows sequence similarity to homo sapiens cDNA FLJ20116 fis, clone COLO 5655 and homo sapiens cDNA FLJ20740 fis, clone HEP07118.

SEQ ID NO: 1051 is the determined cDNA sequence for clone C883P which shows sequence similarity to human homeobox protein Cdx2 mRNA.

SEQ ID NO: 1052 is the determined cDNA sequence for clone C884P which shows sequence similarity to human TM4SF3 (aka, CO-029).

SEQ ID NO: 1053 is the determined cDNA sequence for clone C886P which shows sequence similarity to human secretory protein (P1.B) mRNA and homo sapiens trefoil factor 3 (intestinal) (TFF3) mRNA.

SEQ ID NO: 1054 is the determined cDNA sequence for clone C892P which shows sequence similarity to human galectin-4 mRNA.

SEQ ID NO: 1055 is the determined cDNA sequence for clone C900P which shows sequence similarity to homo sapiens mucin 11 (MUC11) mRNA.

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SEQ ID NO: 1056 is the determined cDNA sequence for clone C902P which shows sequence similarity to homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA.

SEQ ID NO: 1057 is the determined cDNA sequence for clone C903P which shows sequence similarity to homo sapiens transmembrane mucin 12 (MUC12) mRNA.

SEQ ID NO: 1058 is the determined cDNA sequence for clone C899P which shows sequence similarity to homo sapiens intestinal mucin (MUC2) mRNA.

SEQ ID NO:1059 is the predicted amino acid sequence for the clone of SEQ ID NO:1049.

SEQ ID NO:1060 is the predicted amino acid sequence for the clone of SEQ ID NO:1050.

SEQ ID NO:1061 is the predicted amino acid sequence for the clone of SEQ ID NO:1051.

SEQ ID NO:1062 is the predicted amino acid sequence for the clone of SEQ ID NO:1052.

SEQ ID NO:1063 is the predicted amino acid sequence for the clone of SEQ ID NO:1053.

SEQ ID NO:1064 is the predicted amino acid sequence for the clone of SEQ ID NO:1054.

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SEQ ID NO:1065 is the predicted amino acid sequence for the clone of SEQ ID NO:1055.

SEQ ID NO:1066 is the predicted amino acid sequence for the clone of SEQ ID NO:1056.

SEQ ID NO:1067 is the predicted amino acid sequence for the clone of SEQ ID NO:1057.

SEQ ID NO:1068 is the predicted amino acid sequence for the clone of SEQ ID NO:1058.

SEQ ID NO:1069 is the full length nucleotide sequence for clone CS1-152 (C880P, C887P).

SEQ ID NO:1070 is the predicted amino acid sequence for the clone of SEQ ID NO:1069.

SEQ ID NO:1071 is the cDNA sequence for human colon specific gene (geneseq X03195) identified from a computer search of the public geneseq database and which shows similarity to clone C880P.

SEQ ID NO:1072 is the cDNA sequence for human protein comprising secretory signal nucleotide sequence 3 (geneseq V29035) identified from a computer search of the public geneseq database and which shows similarity to clone C880P.

SEQ ID NO:1073 is the cDNA sequence for open reading frame human protein comprising secretory signal 3 (geneseq V29036) identified from a computer search of the public geneseq database and which shows similarity to clone C880P.

SEQ ID NO:1074 is the cDNA sequence for human colon specific protein cDNA (geneseq T51784) identified from a computer search of the public geneseq database and which shows similarity to clone C880P.

SEQ ID NO:1075 is the cDNA sequence for human Reg 1-gamma protein (geneseq V29156) identified from a computer search of the public geneseq database and which shows similarity to clone C880P.

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SEQ ID NO:1076 is the cDNA sequence for human intestinal peptideassociated transporter HPT-1 mRNA, complete cds and homo sapiens mRNA for L1cadherin (geneseq X18166) identified from a computer search of the public geneseq database and which shows similarity to clone C888P.

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SEQ ID NO:1077 is the amino acid sequence of geneseq record W12691 which shows sequence similarity to clone C880P.

SEQ ID NO:1078 is the amino acid sequence of geneseq record W37866 which shows sequence similarity to clone C880P.

SEQ ID NO:1079 is the amino acid sequence of geneseq record W37929 which shows sequence similarity to clone C880P.

SEQ ID NO:1080 is the amino acid sequence of geneseq record W84274 which shows sequence similarity to clone C880P.

SEQ ID NO:1081 is the amino acid sequence of geneseq record W740898 which shows sequence similarity to clone C888P.

SEQ ID NO:1082 is the determined cDNA sequence for clone 27540

SEQ ID NO:1083 is the predicted amino acid sequence of clone 27540 (SEQ ID NO:1082)

DETAILED DESCRIPTION OF THE INVENTION

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As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as colon cancer. The compositions described herein may include colon tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (e.g., T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a colon tumor protein or a variant thereof. A "colon tumor protein" is a protein that is expressed in colon tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain colon tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with colon cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above.

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Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human colon tumor proteins. Sequences of polynucleotides encoding specific tumor proteins are provided in SEQ ID NO: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081.

COLON TUMOR PROTEIN POLYNUCLEOTIDES

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Any polynucleotide that encodes a colon tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a colon tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a colon tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes a colon tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity

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to a polynucleotide sequence that encodes a native colon tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins - Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 20 Methods in Enzymology vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153; Myers, E.W. and Muller W. (1988) CABIOS 4:11-17; Robinson, E.D. (1971) Comb. Theor 11:105; Santou, N. Nes, M. (1987) Mol. Biol. Evol. 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) Numerical Taxonomy - the Principles and Practice of Numerical Taxonomy, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Proc. Natl. Acad., Sci. USA 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference

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sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native colon tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

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It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (i.e., expression that is at least two fold greater in a colon tumor than in normal tissue, as determined

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using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as colon tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a colon tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

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For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

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Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

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One such amplification technique is inverse PCR (see Triglia et al., Nucl. Acids Res. 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., PCR Methods Applic. 1:111-19, 1991) and walking PCR (Parker et al., Nucl. Acids Res. 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

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Certain nucleic acid sequences of cDNA molecules encoding portions of colon tumor proteins are provided in SEQ ID NO: 1-121, 123-197, 205-630, 632-684, 686, 690-691, and 694-1081. These polynucleotides were isolated from colon tumor cDNA libraries using conventional and/or PCR-based subtraction techniques, as described below.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., DNA 2:183, 1983). Alternatively, RNA molecules may be generated by in vitro or in vivo transcription of DNA sequences encoding a colon tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated in vivo (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a colon tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (i.e., an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., In Huber and Carr, Molecular and Immunologic Approaches, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

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A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability in vivo. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetylmethyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

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Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally

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transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

COLON TUMOR POLYPEPTIDES

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Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a colon tumor protein or a variant thereof, as described herein. As noted above, a "colon tumor protein" is a protein that is expressed by colon tumor cells. Proteins that are colon tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with colon cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (i.e., specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a colon tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (e.g., 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

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Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, Fundamental Immunology, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigenspecific" if they specifically bind to an antigen (i.e., they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native colon tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native colon tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native colon tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants

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in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain non-conservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

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Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, J. Am. Chem. Soc. 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

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Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both

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immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

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Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a nonfused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., Gene 40:39-46, 1985; Murphy et al., Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino

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acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997).

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Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in E. coli (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible

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for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

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The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a colon tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a colon tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a colon tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about

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10³ L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as colon cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a colon tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

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Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin

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or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, Eur. J. Immunol. 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

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Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be

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prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

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A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl

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groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

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A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

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nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

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T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a colon tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEXTM system, available from Nexell Therapeutics Inc., Irvine, CA. Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a colon tumor polypeptide, polynucleotide encoding a colon tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a colon tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a colon tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation,

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compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., Cancer Res. 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a colon tumor polypeptide (100 ng/ml - 100 μ g/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-y) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a colon tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Colon tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a colon tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a colon tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a colon tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a colon tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

30 PHARMACEUTICAL COMPOSITIONS AND VACCINES

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Within certain aspects, polypeptides, polynucleotides, T cells and/or

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binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (i.e., vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

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A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated in situ. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, Crit. Rev. Therap. Drug Carrier Systems 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as Bacillus-Calmette-Guerrin) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), 30 replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., Proc. Natl. Acad. Sci. USA 86:317-321, 1989; Flexner et al., Ann. N.Y.

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Acad. Sci. 569:86-103, 1989; Flexner et al., Vaccine 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, Biotechniques 6:616-627, 1988; Rosenfeld et al., Science 252:431-434, 1991; Kolls et al., Proc. Natl. Acad. Sci. USA 91:215-219, 1994; Kass-Eisler et al., Proc. Natl. Acad. Sci. USA 90:11498-11502, 1993; Guzman et al., Circulation 88:2838-2848, 1993; and Guzman et al., Cir. Res. 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., Science 259:1745-1749, 1993 and reviewed by Cohen, Science 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present

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invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

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Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, Ann. Rev. Immunol. 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt.

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MPL adjuvants are available from Corixa Corp. (Seattle, WA) (see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., Science 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

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Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Ribi ImmunoChem Research Inc., Hamilton, MT), RC-529 (Corixa, Seattle, WA) and Aminoalkyl glucosaminide 4-phosphates (AGPs).

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see*, *e.g.* Coombes et al., *Vaccine 14*:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained

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within a reservoir surrounded by a rate controlling membrane.

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Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-coglycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (see e.g., U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects per se and/or to be immunologically compatible with the receiver (i.e., matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their

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ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells in vivo or ex vivo, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., Nature Med. 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated $ex\ vivo$ by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a colon tumor protein (or portion or other variant thereof) such that the colon tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising

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such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs in vivo. In vivo and ex vivo transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., Immunology and cell Biology 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the colon tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unitdose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

CANCER THERAPY

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In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as colon cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor.

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Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic,

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macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term in vivo. Studies have shown that cultured effector cells can be induced to grow in vivo and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al., Immunological Reviews 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated ex vivo for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

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Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (i.e., untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccinedependent generation of cytolytic effector cells capable of killing the patient's tumor cells in vitro. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-

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vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a colon tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

15 METHODS FOR DETECTING CANCER

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In general, a cancer may be detected in a patient based on the presence of one or more colon tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as colon cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a colon tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b)

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detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length colon tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding

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agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

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More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (i.e., incubation time) is a period of time that is sufficient to detect the

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presence of polypeptide within a sample obtained from an individual with colon cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20[™]. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as colon cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered

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positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., Clinical Epidemiology: A Basic Science for Clinical Medicine, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

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In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich

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assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use colon tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such colon tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a colon tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a colon tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated in vitro for 2-9 days (typically 4 days) at 37°C with one or more representative polypeptides (e.g., 5 - 25 μg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of colon tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a colon tumor protein in a biological sample. For

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example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a colon tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the colon tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a colon tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

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To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a colon tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-121, 123-197, 205-630, 632-684, 686, 690-691, and 694-1081. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and

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from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple colon tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

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The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds,

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reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a colon tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a colon tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a colon tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a colon tumor protein.

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The following Examples are offered by way of illustration and not by way of limitation.

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EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF COLON TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION AND MICROARRAY ANALYSIS

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A cDNA library was constructed in the PCR2.1 vector (Invitrogen, Carlsbad, CA) by subtracting a pool of three colon tumors with a pool of normal colon, spleen, brain, liver, kidney, lung, stomach and small intestine using PCR subtraction methodologies (Clontech, Palo Alto, CA). The subtraction was performed using a PCR-based protocol, which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (Mlul, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs, and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

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The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are over-expressed in colon tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

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To characterize the complexity and redundancy of the subtracted library, 96 clones were randomly picked and 65 were sequenced, as previously described. These sequences were further characterized by comparison with the most recent Genbank database (April, 1998) to determine their degree of novelty. No significant homologies were found to 21 of these clones, hereinafter referred to as 11092, 11093, 11096, 11098, 11103, 11174, 11108, 11112, 11115, 11117, 11118, 11134, 11151, 11154, 11158, 11168, 11172, 11175, 11184, 11185 and 11187. The determined cDNA sequences for these clones are provided in SEQ ID NO: 48, 49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101 and 109-111, respectively.

Two-thousand clones from the above mentioned cDNA subtraction library were randomly picked and submitted to a round of PCR amplification. Briefly, 0.5 µl of glycerol stock solution was added to 99.5 µl of pcr MIX (80 µl H₂0, 10 µl 10X PCR Buffer, 6 µl 25 mM MgCl₂, 1 µl 10 mM dNTPs, 1 µl 100 mM M13 forward primer (CACGACGTTGTAAAACGACGG), 1 µl 100 mM M13 reverse primer (CACAGGAAACAGCTATGACC)), and 0.5 µl 5 u/ml Taq polymerase (primers provided by (Operon Technologies, Alameda, CA). The PCR amplification was run for thirty cycles under the following conditions: 95°C for 5 min., 92°C for 30 sec., 57°C for 40 sec., 75°C for 2 min. and 75°C for 5 minutes.

mRNA expression levels for representative clones were determined using microarray technology (Synteni, Palo Alto, CA) in colon tumor tissues (n=25), normal colon tissues (n=6), kidney, lung, liver, brain, heart, esophagus, small intestine, stomach, pancreas, adrenal gland, salivary gland, resting PBMC, activated

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PBMC, bone marrow, dendritic cells, spinal cord, blood vessels, skeletal muscle, skin, breast and fetal tissues. The number of tissue samples tested in each case was one (n=1), except where specifically noted above; additionally, all the above-mentioned tissues were derived from humans. The PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, and fluorescent-labeled cDNA probes were generated by reverse transcription according to the protocol provided by Synteni. The microarrays were probed with the labeled cDNA probes, the slides scanned, and fluorescence intensity was measured. This intensity correlates with the hybridization intensity.

One hundred and forty nine clones showed two or more fold over-expression in the colon tumor probe group as compared to the normal tissue probe group. These cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A and/or Model 377 (Foster City, CA). These sequences were compared to known sequences in the most recent GenBank database. No significant homologies to human gene sequences were found in forty nine of these clones, represented by the following sixteen cDNA consensus sequences: SEQ ID NO: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46 and 47, hereinafter referred to as Contig 2, 8, 13, 14, 20, 23, 29, 31, 35, 32, 36, 38, 41, 42, 50 and 51, respectively). Contig 29 (SEQ ID NO: 30) was found to be a Rat GSK-3-β-interacting protein Axil homolog. Also, Contigs 31 and 35 (SEQ ID NO: 32 and 33, respectively) were found to be a Mus musculus GOB-4 homolog. The determined cDNA sequences of SEQ ID NO: 1, 3-7, 9-14, 17-21, 23, 25-29, 31, 35, 37, 39, 42-45, 50, 51, 53, 55-58, 61-64, 70-78, 80-88, 91, 92, 94-98, 102-108 and 112 were found to show some homology to previously identified genes sequences.

Microarray analysis demonstrated Contig 2 (SEQ ID NO: 2) showed over-expression in 34% of colon tumors tested, as well as increased expression in normal pancreatic tissue, with no over-expression in normal colon tissues. Upon further analysis, Contigs 2, 8 and 23 were found to share homology to the known gene GW112. Contigs 4, 5, 9 and 52 showed homology to carcinoembryonic antigen (SEQ ID NO: 3, 4, 5 and 6, respectively). A representative sampling of these fragments

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showed over-expression in 85% of colon tumors, with over-expression in normal bone marrow and 3/6 normal colon tissues. Contig 6 (SEQ ID NO: 7), showing homology to the known gene sequence for villin, and was over-expressed in about half of all colon tumors tested, with a limited degree of low level over-expression in normal colon. Contig 12 (SEQ ID NO: 14), showing homology to Chromosome 17, clone hRPC.1171 I 10, also referred to as C798P, was over-expressed in approximately 70% of colon tumors tested, with low over-expression in 1/6 normal colon samples. Contig 14, also referred to as 14261 (SEQ ID NO: 16), showing no significant homology to any known gene, showed over-expression in 44% of colon tumors tested, with low level expression in half of normal colon tissues, as well as small intestine and pancreatic tissue. Contig 18 (SEQ ID NO: 21), showing homology to the known gene for L1-cadherin, showed over-expression in approximately half of colon tumors and low level over-expression in 3/6 normal colon tissues tested. Contig 22 (SEQ ID NO: 23), showing homology to Bumetanide-sensitive Na-K-Cl cotransporter was over-expressed in 70% of colon tumors and no over-expression in all normal tissues tested. Contig 25 (SEQ ID NO: 25), showing homology to macrophage inflammatory protein-3α, was over-expressed in over 40% of colon tumors and in activated PBMC. Contigs 26 and 48 (SEQ ID NOS: 25 and 26), showing homology to the sequence for laminin, was over-expressed in 48% of colon tumors and with low over-expression in stomach tissue. Contig 28 (SEQ ID NO: 29), showing homology to the known gene sequence for Chromosome 16 BAC clone CIT987SK-A-363E6, was over-expressed in 33% of colon tumors tested with normal stomach and 2/6 normal colon tissues showing low level over-expression. Contigs 29, 31 and 35 (SEQ ID NOS: 30, 32 and 33, respectively), also referred to as C751P, an unknown sequence showing limited and partial homology to Rat GSK-3\beta-interacting protein Axil homolog, and Mus musculus GOB-4 homolog, was over-expressed in 74% of colon tumors and no overexpression in all normal tissues tested. Contig 34 (SEQ ID NO: 35), showing homology to the known sequence for desmoglein 2, was over-expressed in 56% of colon tumors and showed low level over-expression in 1/6 normal colon tissues. Contig 36 (SEQ ID NO: 36), an unknown sequence also referred to as C793P, showed over-expression in 30% of colon tumor tissues tested. Contig 37 and 14287.2 (SEQ

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ID NOS: 37 and 116), an unknown sequence, but with limited (89%) homology to the known sequence for putative transmembrane protein was over-expressed in 70% of colon tumors, as well as in normal lung tissue and 3/6 normal colon tissues tested. Contig 38, also referred to as C796P and 14219 (SEQ ID NO: 38), showing no significant homology to any known gene, was over-expressed in 38% in colon tumors and no elevated over-expression in any normal tissues. Contig 41 (SEQ ID NO: 40), also referred to as C799P and 14308, an unknown sequence showing no significant homology to any known gene, was over-expressed in 22% of colon tumors. Contig 42, (SEQ ID NO: 41), also referred to as C794P and 14309, an unknown sequence with no significant homology to any known gene, was over-expressed in 63% of colon tumors tested, as well as in 3/6 normal colon tissues. Contig 43 (SEQ ID NO: 42), showing homology to the known sequence for Chromosome 1 specific transcript KIAA0487 was over-expressed in 85% of colon tumors tested and in normal lung and 4/6 normal colon tissues. Contig 49 (SEQ ID NO: 45), showing homology to the known sequence for pump-1, was over-expressed in 44% of colon tumors and no over-expression in all normal tissues tested. Contig 50 (SEQ ID NO: 46), also referred to as C792P and 18323, showing no significant homology to any known gene, was over-expressed in 33% of colon tumors with no detectable over-expression in any normal tissues tested. Contig 51 (SEQ ID NO: 47), also referred to as C795P and 14317 was over-expressed in 11% of colon tumors.

Additional microarray analysis yielded seven clones showing two or more fold over-expression in the colon tumor probe group as compared to the normal tissue probe group. Three of these clones demonstrated particularly good colon tumor specificity, and are represented by SEQ ID NO: 115, 116 and 120. Specifically, SEQ ID NO: 115, referred to as C791P or 14235, which shows homology to the known gene sequence for H. sapiens chromosome 21 derived BAC containing ets-2 gene, was over-expressed in 89% of colon tumors tested and in 5/6 normal colon tissues, as well as over-expressed at low levels in normal lung and activated PBMC. Microarray analysis for SEQ ID NO: 116 is discussed above. SEQ ID NO: 120, referred to as 14295, showing homology to the known gene sequence for secreted cement gland protein XAG-2 homolog, was over-expressed in 70% of colon tumors and in 5/6

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normal colon tissues, as well as low level over-expression in normal small intestine, stomach and lung. All clones showing over-expression in colon tumor were sequenced and these sequences compared to the most recent Genbank database (February 12, 1999). Of the seven clones, three contained sequences that did not share significant homology to any known gene sequences, represented by SEQ ID NO: 116, 117 and 119. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in colon. The determined cDNA sequences of the remaining clones (SEQ ID NO: 113-115 and 120) were found to show some homology to previously identified genes.

Further analysis identified a clone which was recovered several times by PCR subtraction and by expression screening using a mouse anti-scid antiserum. The determined full length cDNA sequence for this clone is provided in SEQ ID NO: 121, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 122. This clone is homologous with the known gene Beta IG-H3, as disclosed in U.S. Patent No. 5,444,164. Microarray analysis demonstrated this clone to be overexpressed in 75 to 80% of colon tumors tested (n=27), with no over-expression in normal colon samples (n=6), but with some low level over-expression in other normal tissues tested.

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Further analysis of the PCR-subtraction library described above led to the isolation of longer cDNA sequences for the clones of SEQ ID NO: 30, 115, 46, 118, 41, 47, 38, 113, 14 and 40 (known as C751P, C791P, C792P, C793P, C794P, C795P, C796P, C797P, C798P and C799P, respectively). These determined cDNA sequences are provided in SEQ ID NO: 123-132, respectively. Additional sequences for the clones C794P and C799P are shown in SEQ ID NO:683 and 684, respectively, and the predicted amino acid sequences are shown in SEQ ID NO:685 and 686, respectively. Still further sequences for the clones C794P and C799P are shown in SEQ ID NO: 691 and 690, respectively, and to the predicted amino acid sequence as shown in SEQ ID NO: 693 and 692, respectively.

Using PCR subtraction methodology described above with minor modifications, transcripts from a pool of three moderately differentiated colon adenocarcinoma samples were subtracted with a set of transcripts from normal brain,

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pancreas, bone marrow, liver, heart, lung, stomach and small intestine. Modifications of the above protocol were included at the cDNA digestion steps and in the tester to drive hybridization ratios. In a first subtraction, the restriction enzymes PvuII, DraI, MscI and StuI were used to digest cDNAs, and the tester to driver ratio was 1:40, as suggested by Clontech. In a second subtraction, DraI, MscI and StuI were used for cDNA digestion and a tester to driver ratio of 1:76 was used. Following the PCR amplification steps, the cDNAs were clones into pCR2.1 plasmid vector. determined cDNA sequences of 167 isolated clones are provided in SEQ ID NO: 205-371. These sequences were compared to sequences in the public databases as described above. The sequences of SEQ ID NO: 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369 and 371 were found to show some homology to previously identified ESTs. remaining sequences were found to show some homology to previously identified genes.

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Using the PCR subtraction technology described above, a cDNA library from a pool of primary colon tumors was subtracted with a cDNA library prepared from normal tissues, including brain, bone marrow, kidney, heart, lung, liver, pancreas, small intestine, stomach and trachea. The determined cDNA sequences for 90 clones isolated in this subtraction are provided in SEQ ID NO: 372-461. Comparison of these sequences with those in the public databases as described above, revealed no homologies to the sequences of SEQ ID NO: 426, 445 and 453. The sequences of SEQ ID NO: 372-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455 and 457-461 showed some homology to previously identified genes, while the sequences of SEQ ID NO: 379, 405, 407, 408, 418, 424, 430-432, 437, 442, 444, 452 and 456 showed some homology to previously isolated ESTs.

Using the PCR subtraction methodology described above, a cDNA library prepared from a pool of metastatic colon tumors was subtracted with cDNA from a pool of normal tissues, namely brain, heart, lung, lymph nodes, PBMC,

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pancreas, small intestine and stomach. The determined cDNA sequences for 82 clones isolated from the subtracted library are provided in SEQ ID NO: 487-568 (referred to as contigs 1-56 and 58-83, respectively). The sequences of SEQ ID NO: 487, 489, 490, 493-496, 499, 501-509, 511-518, 520-526, 529-542, 544, 546, 548-552, 554, 555, 557, 558, 560, 562, 563, 566 and 567 showed some homology to previously identified gene sequences. The sequences of SEQ ID NO: 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 559, 564, 564 and 568 showed some homology to previously isolated ESTs.

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Example 2

ISOLATION OF TUMOR POLYPEPTIDES USING SCID MOUSE-PASSAGED TUMOR RNA

Human colon tumor antigens were obtained using SCID mouse passaged colon tumor RNA as follows. Human colon tumor was implanted in SCID mice and harvested, as described in Patent Application Serial No. 08/556,659 filed 11/13/95, U.S. Patent No. 5,986,170. First strand cDNA was synthesized from poly A+ RNA from three SCID mouse-passaged colon tumors using a Lambda ZAP Express cDNA synthesis kit (Stratagene). The reactions were pooled and digested with RNase A, T1 and H to cleave the RNA and then treated with NaOH to degrade the RNA. The resulting cDNA was annealed with biotinylated (Vector Labs, Inc., Burlingame, CA) cDNA from a normal resting PBMC plasmid library (constructed from Superscript plasmid System, Gibco BRL), and subtracted with streptavidin by phenol/chloroform extraction. Second strand cDNA was synthesized from the subtracted first strand cDNA and digested with S1 nuclease (Gibco BRL). The cDNA was blunted with Pfu polymerase and EcoRI adaptors (Stratagene) were ligated to the ends. The cDNA was phosphorylated with T4 polynucleotide kinase, digested with restriction endonuclease XhoI, and size selected with Sephacryl S-400 (Sigma). Fractions were pooled, ligated to Lambda ZAP Express arms (Stratagene) and packaged with Gigapack Gold III extract (Stratagene). Random plaques were picked,

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phagemid was excised, transformed into XLOLR cells (Stratagene) and resulting plasmid DNA (Qiagen Inc., Valencia, CA) was sequenced as described above.

The determined cDNA sequences for 17 clones isolated as described above are provided in SEQ ID NO: 133-151, wherein 133 and 134 represent partial sequences of a clone referred to as CoSub-3 and SEQ ID NO: 135 and 136 represent partial sequences of a clone referred to as CoSub-13. These sequences were compared with those in the public databases as described above. The sequences of SEQ ID NO: 139 and 149 showed no significant homologies to any previously identified sequences. The sequences of SEQ ID NO: 138, 140, 141, 142, 143, 148 and 149 showed some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 133-137, 144-147, 150 and 151 showed some homology to previously isolated gene sequences.

The determined cDNA sequences for an additional 46 clones isolated as described above, are provided in SEQ ID NO: 569-616, wherein SEQ ID NO: 573 and 574 represent the 3' and 5' determined cDNA sequences, respectively, for clone CS1-106, and SEQ ID NO: 579 and 580 represent the determined 3' and 5' cDNA sequences, respectively, for clone CS1-124. Comparison of the isolated sequences with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 580, 585, 610 and 613. The sequences of SEQ ID NO: 569, 574-577, 584, 587, 592, 595, 598, 603 and 608 showed some homology to previously isolated ESTs, while the sequences of SEQ ID NO: 570-573, 578, 581-583, 586, 588-591, 593, 594, 596, 597, 599-602, 604-607, 609, 611, 612 and 514-616 showed some homology to previously isolated gene sequences.

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Example 3

USE OF MOUSE ANTISERA TO IDENTIFY DNA SEQUENCES ENCODING COLON TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding colon tumor antigens by screening of colon tumor cDNA libraries with mouse antitumor sera.

A cDNA expression library was prepared from SCID mouse-passaged

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human colon tumor poly A+ RNA using a Stratagene (La Jolla, CA) Lambda ZAP Express kit, following the manufacturer's instructions. Sera was obtained from the colon tumor-bearing SCID mouse. This serum was injected into normal mice to produce anti-colon tumor serum. Approximately 600,000 PFUs were screened from the unamplified library using this antiserum. Using a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (BRL Labs.), positive plaques were identified. Phage was purified and phagemid excised for several clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined cDNA sequences for 46 of the isolated clones are provided in SEQ ID NO: 152-197. The predicted amino acid sequences for the cDNA sequences of SEQ ID NO: 187, 188, 189, 190, 194, 195 and 197 are provided in SEQ ID NO: 198-204, respectively. The determined cDNA sequences were compared with those in the public database as described above. The sequences of SEQ ID NO: 156, 168, 184, 189, 192 and 196 showed some homology to previously isolated ESTs. The sequences of SEQ ID NO: 152-155, 157-167, 169-182, 183, 185-188, 190, 194, 195 and 197 showed some homology to previously identified genes.

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The determined cDNA sequences for an additional eleven clones isolated as described above, are provided in SEQ ID NO: 617-627. Comparison of these sequences with those in the public database as described above revealed no known homologies to SEQ ID NO: 621 and 623. The sequences of SEQ ID NO: 622 and 626 were found to show some homology to previously isolated ESTs, while the sequences of SEQ ID NO: 617-620, 624, 625 and 627 showed some homology to previously identified genes.

In further studies, a cDNA library was prepared from SCID-mouse grown colon tumors and screened with mouse anti-SCID serum as described above. Briefly first strand cDNA was synthesized from poly A+ RNA from three SCID mouse-grown human colon tumors using a Lambda ZAP Express cDNA synthesis kit (Stratagene). The reactions were pooled and digested with RNase A, T1 and H to 30 cleave the RNA and then treated with NaOH to degrade the RNA. The cDNA was annealed with biotinylated cDNA from a normal resting PBMC plasmid library

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(constructed from Superscript plasmid system; Gibco BRL) and subtracted with streptavidin by phenol/chloroform extraction. Second strand cDNA was synthesized from the subtracted first strand cDNA and digested with S1 nuclease. The cDNA was blunted with Pfu polymerase and EcoRI adaptors were ligated to the ends. The cDNA was phosphorylated with T4 polynucleotide kinase, digested with restriction endonuclease XhoI, and size selected with Sephacryl S-400 (Sigma). Fractions were pooled, ligated to Lambda ZAP Express arms (Stratagene) and packaged with Gigapack Gold III extract (Stratagene). The resulting library was screened with a mouse antiserum raised against serum from SCID mice containing human colon tumors, including the three tumors used to prepare the cDNA libraries.

The determined cDNA for one clone isolated using this procedure is provided in SEQ ID NO: 630. This clone was found to show homology to a previously identified gene. The amino acid sequence encoded by the clone of SEQ ID NO: 630 is provided in SEQ ID NO: 631.

In subsequent studies, an additional cDNA library was prepared from a SCID-passaged human colon tumor and screened with a mouse antiserum raised against serum from the SCID mouse containing the colon tumor. The determined cDNA sequences for 51 clones isolated in these studies are provided in SEQ ID NO: 632-682. Comparison of these sequences with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 648 and 668. The sequence of SEQ ID NO: 642 showed some homology to previously isolated ESTs. The sequences of SEQ ID NO: 632-641, 643-647, 649-667 and 669-682 were found to show some homology to previously identified genes. SEQ ID NO: 684 and SEQ ID NO: 690 showed homology to human NADH/NADPH thyroid oxidase p138-tox mRNA.

Example 4

ISOLATION AND CHARACTERIZATION OF COLON TUMOR POLYPEPTIDES BY CONVENTIONAL SUBTRACTION

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Two cDNA libraries were constructed and used to create a subtracted cDNA library as follows.

Using the GibcoBRL Superscript Plasmid System with minor modifications, two cDNA libraries were created. The first library, referred to as CTCL, was prepared from a pool of mRNA samples from three colon adenocarcinoma tissue samples. Two of the samples were described as Duke's stage C and one as Duke's stage B. All three samples were grade III in histological status. A second library (referred to as DriverLibpcDNA3.1+) was prepared from a pool of normal tissues, namely liver, pancreas, skin, bone marrow, resting PBMC, stomach and brain. Both libraries were prepared using the manufacturer's instructions with the following modifications: an EcoRI-NotI 5' cDNA adapter was used instead of the provided reagent; the vector pCDNA3.1(+) (Invitrogen) was substituted for the pSPORT vector; and the ligated DNA molecules were transformed into ElectroMaxDH10B electrocompetent cells. Clones from the libraries were analyzed by restriction digest and sequencing to determine average insert size, quality of the library and complexity of the library. DNA was prepared from each library and digested.

The driver DNA was biotinylated and hybridized with the colon library tester DNA at a ratio of 10:1. After two rounds of hybridizations, streptavidin incubations and extractions, the remaining colon cDNAs were size-selected by column chromatography and cloned into the pCMV-Script vector from Stratagene. Clones from this subtracted library (referred to as CTCL-S1) were characterized as described above for the unsubtracted libraries.

The determined cDNA sequences for 20 clones isolated from the CTCL-S1 library are provided in SEQ ID NO: 462-479, 628 and 629. Comparison of these sequences with those in the public databases, as described above, revealed no significant homologies to the sequences of SEQ ID NO: 476, 477 and 479. The remaining sequences showed some homology to previously identified genes.

In further studies, a cDNA library was prepared from a pool of mRNA from three metastatic colon adenocarcinomas derived from liver tissue samples. All samples were described as Duke's stage D. Conventional subtraction was performed as described above, using the DriverLibpcDNA3.1+ library described above as the

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driver. The resulting subtracted library (referred to as CMCL-S1) was characterized by isolating a set of clones for restriction analysis and sequencing.

The determined cDNA sequences for 7 clones isolated from the CMCL-S1 library are provided in SEQ ID NO: 480-486. Comparison of these sequences with those in the public databases revealed no significant homologies to the sequence of SEQ ID NO: 483. The sequences of SEQ ID NO: 480-482 and 484-486 were found to show some homology to previously identified genes.

Example 5

SYNTHESIS OF POLYPEPTIDES

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Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

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CLAIMS

1. An isolated polypeptide, comprising at least an immunogenic 10 portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 15 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 25 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081;

> (b) sequences that hybridize to a sequence recited in any one of SEO ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-

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193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and

(c) complements of sequences of (a) or (b).

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- 2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081, or a complement of any.of the foregoing polynucleotide sequences.
- 3. An isolated polypeptide comprising a sequence recited in any one of SEO ID NOs: 122 and 198-204.

- An isolated polynucleotide encoding at least 15 amino acid residues of a colon tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID Nos: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081, or a complement of any of the foregoing sequences.
- 5. An isolated polynucleotide encoding a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-

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691, and 694-1081, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-10 378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081.

- 7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081 under moderately stringent conditions.
- 30 8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

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- 9. An expression vector, comprising a polynucleotide according to any one of claims claim 4-8.
- 10. A host cell transformed or transfected with an expression vector according to claim 9.

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- 11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a colon tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:_2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081, or a complement of any of the foregoing polynucleotide sequences.
 - 12. A fusion protein, comprising at least one polypeptide according to claim 1.

13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of

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claim 1.

15. A fusion protein according to claim 12, wherein the fusion protein comprises an affinity tag.

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- 16. An isolated polynucleotide encoding a fusion protein according to claim 12.
- 17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:
 - (a) a polypeptide according to claim 1;
 - (b) a polynucleotide according to claim 4;
 - (c) an antibody according to claim 11;
 - (d) a fusion protein according to claim 12; and
 - (e) a polynucleotide according to claim 16.
 - 18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:
 - (a) a polypeptide according to claim 1;
 - (b) a polynucleotide according to claim 4;
 - (c) an antibody according to claim 11;
 - (d) a fusion protein according to claim 12; and
 - (e) a polynucleotide according to claim 16.
- 25 19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.
 - 20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.
 - 21. A method for inhibiting the development of a cancer in a

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patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

- 22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 18.
- A pharmaceutical composition comprising an antigen presenting cell that expresses a polypeptide according to claim 1, in combination with
 a pharmaceutically acceptable carrier or excipient.
 - 24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.
- 25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (a) sequences recited in SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081;
 - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and
 - (c) complements of sequences of (i) or (ii); in combination with an immunostimulant.

- 26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.
- 30 27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

- 28. A vaccine according to claim 25, wherein the antigenpresenting cell is a dendritic cell.
- 29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (a) sequences recited in SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081;
 - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and
 - (c) complements of sequences of (i) or (ii)encoded by a polynucleotide recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081;

and thereby inhibiting the development of a cancer in the patient.

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- 30. A method according to claim 29, wherein the antigenpresenting cell is a dendritic cell.
- 31. A method according to any one of claims 21, 22 and 29, wherein the cancer is colon cancer.
 - 32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a colon tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (i) polynucleotides recited in any one of SEQ ID NOs: 1-

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121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

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- 33. A method according to claim 32, wherein the biological sample is blood or a fraction thereof.
- 34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.
 - 35. A method for stimulating and/or expanding T cells specific for a colon tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:
 - (a) polypeptides comprising at least an immunogenic portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- 20 (i) sequences recited in SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081;
 - (ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and

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- (iii) complements of sequences of (i) or (ii);
- (b) polynucleotides encoding a polypeptide of (a); and
- (c) antigen presenting cells that express a polypeptide of (a);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

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36. An isolated T cell population, comprising T cells prepared

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according

to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

- 38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:
- (a) incubating CD4⁺ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of:
 - (i) polypeptides comprising at least an immunogenic portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (1) sequences recited in SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081
 - (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and
 - (3) complements of sequences of (1) or (2);
 - (ii) polynucleotides encoding a polypeptide of (i); and
 - (iii) antigen presenting cells that expresses a polypeptide of

(i);

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such that T cells proliferate; and

- (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.
- 39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:
 - (a) incubating CD4+ and/or CD8+ T cells isolated from a patient

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with at least one component selected from the group consisting of:

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and

- (i) polypeptides comprising at least an immunogenic portion of a colon tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (1) sequences recited in SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081;
 - (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 under moderately stringent conditions; and
 - (3) complements of sequences of (1) or (2);
 - (ii) polynucleotides encoding a polypeptide of (i); and
 - (iii) antigen presenting cells that express a polypeptide of (i); such that T cells proliferate;
- (b) cloning at least one proliferated cell to provide cloned T cells;
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.
- 40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
 - (a) contacting a biological sample obtained from a patient with a binding agent that binds to a colon tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 or a complement of any of the foregoing polynucleotide sequences;
 - (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-30 off value, and therefrom determining the presence or absence of a cancer in the patient.

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- 41. A method according to claim 40, wherein the binding agent is an antibody.
- 5 42. A method according to claim 43, wherein the antibody is a monoclonal antibody.
 - 43. A method according to claim 40, wherein the cancer is colon cancer.

- 44. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a colon tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 or a complement of any of the foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of polypeptide that binds to 20 the binding agent;
 - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in
 the patient.
 - 45. A method according to claim 44, wherein the binding agent is an antibody.
- 30 46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

- 47. A method according to claim 44, wherein the cancer is a colon cancer.
- 48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a colon tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 or a complement of any of the foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.
- 49. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.
- 50. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.
 - 51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient with an
 30 oligonucleotide that hybridizes to a polynucleotide that encodes a colon tumor protein,
 wherein the tumor protein comprises an amino acid sequence that is encoded by a

polynucleotide sequence recited in any one of SEQ ID NOs: 1-121, 123-197, 205-630 and 632-684, 686, 690-691, and 694-1081 or a complement of any of the foregoing polynucleotide sequences;

- (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;
 - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polynucleotide detected in step (c) to
 the amount detected in step (b) and therefrom monitoring the progression of the
 cancer in the patient.
 - 52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

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53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

- 54. A diagnostic kit, comprising:
- (a) one or more antibodies according to claim 11; and
- (b) a detection reagent comprising a reporter group.
- 55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.
 - 56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.
- 30 57. A kit according to claim 54, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent

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groups, enzymes, biotin and dye particles.

- 58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a colon tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081, or a complement of any of the foregoing polynucleotides.
- 59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648, 668, 682-684, 686, 690-691, and 694-1081.

- 60. A diagnostic kit, comprising:
- (a) an oligonucleotide according to claim 59; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or
- 5 hybridization assay.

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SEQUENCE LISTING

<110> Corixa Corporation Xu, Jiangchun Lodes, Michael J. Secrist; Heather Benson, Darin R. Meagher, Madeleine Joy King, Gordon E. <120> COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE <130> 210121.47101PC <140> PCT <141> 2000-12-29 <160> 1083 <170> FastSEQ for Windows Version 3.0 <210> 1 <211> 458 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1) ... (458) <223> n = A, T, C or Gncaggtctgg cggcacctgt gcactcagcc gtcgatacac tggtcgattg ggacagggaa 60 gacgatgtgg ttttcaggga ggcccagaga tttggagaag cggatgaagt tctcctttag 120 ttccqaaqtc agctccttqq ttctcccqta qagqqtqatc ttqaaqtact ccctqttttq 180 agaaactttc ttgaagaaca ccatagcatg ctggttgtag ttggtgctca ccactcggac 240 gaggtaactc gttaatccag ggtaactctt aatgttgccc agcgtgaact cgccgggctg 300 qcaacctgga acaaaagtcc tgatccagta gtcacacttc tttttcctaa acaggacgga 360 ggtgacattg tagctcttgt cttctttcag ctcatagatg gtggcataca tcttttgcgg 420 458 gtctttgtct tctctgagaa ttgcattccc tgccagga <210> 2 <211> 423 <212> DNA <213> Homo sapien <400> 2 cagggtccat aggtgatccg caactctcga gcatttatat acaatagcaa atcatccagt 60 gtgttgtaca gtctataata ctccaacagt ctcccatctg tattcaatgg cgccacccaa 120

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240

PCT/US00/35596

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                                                                   1151
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aattccacat ttgggatagg tcctctctgg aagtgaatgt caggcagtga catccaagtt
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                                                                       120.
caaaataaaa gtaactgttt acgttggtga
                                                                       150
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      <211> 403
      <212> DNA
      <213> Homo sapien
      <400> 14
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                                                                       240
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                                                                       300
gcataggtga gccctgagca ctaaaaggag gggtccctga agctttccca ctatagtgtg
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gagttctgtc cctgaggtgg gtacagcagc cttggttcct ctg
                                                                       403
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caaaagcaca gaagcacatc acatacacca gcaaggtttc caactactgc actgattaac
                                                                       180
tagatactct caatagcttt tctatagctc qtcctaqaaa aaaaaattaa attttcattt
                                                                       240
tcttacaagt tccaggctta aacaaaggca aaaattacat qcaacaactg atacactcat
                                                                       300
aagttgcaca tatgctccaa ggtctttatt agataacaat aaatgctagc actttgtcac
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tgccatcaga ttttccttat agtcttagag tcatgtaaat aaaagttcca taatqaaatt
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caaatggtat gtttttcagt acagttggat gtcgtcctac aagatgtggt gaatttgaaa
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                                                                       240
catctgtcac aataagncgt gaacttggca aaagaacttg cattgtactt cacaccaaac
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      <210> 22
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gagcagccac ctacttcaaa cccagcaccc gcagattgtg caggctgcgt cttcagcacc
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      <213> Homo sapien
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gaagtttggc tggatcaagg gtgtattagt acgttgtatg ttaaacattt ggggtgtgat
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                                                                       240
aataatgatg g
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      <211> 421
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      <220>
      <221> misc feature
      <222> (1)...(421)
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                                                                      120
ccqqctcccq tqqatqamcq yqqqacctqy caswqctcct qtktycctqc yagsacacca
                                                                      180
cnytttyccg tggacacrar kggaacckct tggaattcac agctyatgtt ctttctcara
                                                                      240
agtttgagaa agaactttct aaagtgaggg aatatgtcca attaattagt gtgtatgaaa
                                                                      300
agaaactgtt aaacctaact gteegaattg acateatgga raaaggatac catttettac
                                                                      360
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                                                                      421
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                                                                       120
ttaaaaaata gcttgttgct tgcaanaaag tccatataat cttattcccc cccaaatata
                                                                       180
attttatact ttgcactaaa ccaaaatagc ttatggaaaa ttagtattaa atagctaaac
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acagaaaacc tacagctata aataacataa aatacagttt aactttaatg ngatgcttaa
                                                                       300
acaaagcaaa ctatgatgca atatgaatca acttcattaa ttggacaagt ccagnggagg
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cacaaattag ataagcacta a
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                                                                       120
gaaggttgat accagaagcc aagaacgctg gggttacaat ccaagacaca ctcaacacat
                                                                       180
                                                                      240
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gcnacttgcn ggccaaggaa ggcanaactn ggaanaaaag gccccttaag caaaagggnc
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                                                                      401
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9

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<223> n = A,T,C or G <400> 27
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aattgcaact ggacttttat tgggcagtta cnacaacnaa tgttttcana aaaatatttg 60 gaaaaaatat accacttcat agctaagtct tacagagaan aggatttgct aataaaactt 120 aagttttgaa aattaagatg cnggtanagc ttctgaacta atgcccacag ctccaaggaa 180 nacatgtcct atttagttat tcaaatacca gttgagggca ttgtgattaa gcaaacaata 240 tatttgttan aactttgntt ttaaattact gntncttgac attacttata aaggagnctc 1300 taactttcga tttctaaaac tatgtaatac aaaagtatan ntttccccat tttgataaaa 360 gggccnanga tactgantag gaa

<210> 28

<211> 401

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (401)

<223> n = A, T, C or G

<400> 28

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<210> 29

<211> 401

<212> DNA

<213> Homo sapien

<400> 29

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<210> 30

<211> 401

<212> DNA

<213> Homo sapien

<400> 30

cctgaactat ttattaaaaa catgaccact cttggctatt gaagatgctg cctgtatttg 60 agagactgcc atacataata tatgacttcc tagggatctg aaatccataa actaagagaa 120 actgtgtata gcttacctga acaggaatcc ttactgatat ttatagaaca gttgatttcc 180 cccatcccca gtttatggat atgctgcttt aaacttggaa gggggagaca ggaagtttta 240 attgttctga ctaaacttag gagttgagct aggagtgcgt tcatggttc ttcactaaca 300 gaggaattat gctttgcact acgtccctcc aagtgaagac agactgttt agacagactt ttaaaaatgg tgccctacca ttgacacatg cagaaattgg t

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<210> 32 <211> 401 <212> DNA <213> Homo sap	ien				
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<210> 34 <211> 401 <212> DNA <213> Homo sar	ien				
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<210> 35 <211> 401 <212> DNA <213> Homo sap	ien				

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<220>
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      <222> (1) ... (401)
      <223> n = A, T, C \text{ or } G
      <400> 35
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                                                                       120
gggtaaagcc tttggcgccc tttccgcaat ggcacatcag cagtaaaagt ggtaccaata
                                                                       180
gcangaacag aaagggcaaa atcatgancg caattgctgc gggtcccaag cccacatagg
                                                                       240
aatcatgctg ngcttccctg cancegctgc catgcaagac actnacaaac tgngantgta
                                                                       300
aggacetget tttcaggaca actaaaacce tgattgnetg aaatcaggaa etgaatttea
                                                                       360
cttctcccaa gctttttctc actttggtgc aacancacac t
                                                                       401
      <210> 36
      <211> 401
      <212> DNA
      <213> Homo sapien
      <400> 36
cctgctagaa tcactgccgc tgtgctttcg tggaaatgac agttccttgt tttttttgtt
                                                                        60
tctgtttttg ttttacatta gtcattggac cacagccatt caggaactac cccctgcccc
                                                                       120
acaaagaaat gaacagttgt agggagaccc agcagcacct ttcctccaca caccttcatt
                                                                       180
ttgaagttcg ggtttttgtg ttaagttaat ctgtacattc tgtttgccat tgttacttgt
                                                                       240
actatacatc tgtatatagt gtacggcaaa agagtattaa tccactatct ctagtgcttg
                                                                       300
actttaaatc agtacagtac ctgtacctgc acggtcaccc gctccgtgtg tcgccctata
                                                                       360
ttgagggctc aagctttccc ttgttttttg aaaggggttt a
                                                                       401
      <210> 37
      <211> 401
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1) ... (401)
      <223> n = A, T, C or G
cnnctntqna atggantnnt tqnctaaaan qanttqatqa tqatqaanat ccctanqanq
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antaagcatg ganchtgatc ntttnctnng cactecttta cgacacggaa acangnatca
                                                                       120
ncatgatggt accaganacc ttatcaccna cgcgcacnga nctgactnat tccaaagagt
                                                                       180
tgnggttacg gncatccggt cattgctcgt qcccattgct qcaqqqctga tnctactqqt
                                                                       240
gettattatg ntggeeetga ggatgeteea caatgaatat aageatgetg catgateage
                                                                       300
ggcaacanat gctctgccgt ttgcactaca tctttcacgg acacnatntc gaanacgggc
                                                                       360
acnttgcana gttagacttg gaatgcatgg ngccggncan n
                                                                       401
      <210> 38
      <211> 401
      <212> DNA
      <213> Homo sapien
      <400> 38
aattggctca ctctctcaag gcaagcactg tctcaaggca gtctcaaggc agagatgaca
                                                                        60
cagcaaaaaa cagaggggga gaaaaaagtc tattattggc ttgtgattta caaaagccaa
                                                                       120
agtectttag ataaaaggee aggagtegta eeaacataga taccaaatee aggagaacae
                                                                       180
agaccagega taagagggae getteeceat gacceagace ageetaaage eeetgtgggg
                                                                       240
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gcagccagtg gggagctgtc agaccttgga catggtggtc tttgagaatg ggtc tctctccctg accagttggg atagacacct gactggaatc cttgacactg gcagctatgaacag agaggactgt gcctgtcttc ctgaatccca a	
<210> 39 <211> 401 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(401) <223> n = A,T,C or G	
<pre><400> 39 tctggtangg agcaattcta ttatttggca ttgcatggct gggttgaatt aaaa gtgagaacag gtgagtctag aagtccaact ctgaaaagga ccactgtaca ttt cggctgtgtt aaagatgctg ctaatgtcag tcactgggtg cactaaagga tct tatgtaaaac gttgggaatg acaagatana actgatactc tggtaagtta ccc ctacttcttg tgaaatacta atgacagcat catcctgcca agcgaaagag gca gcaaggacaa attaaaaggg ggtaagagcc ttatcatgat gaggagtctt gtt cttgggaaaa gctgtccata gtgtgaagtc gtcaatttct c</pre>	gaacaca120cttattt180tctgaag240ggcataa300
<210> 40 <211> 401 <212> DNA <213> Homo sapien	
<pre><400> 40 tctggtcacc caactcttgt ggaagagggg aattgagate gagtactgaa tat agaggetgga atcettcage cccagagece agggaccact ccagtagatg cag cctgcccagg ggtcagggca gtgggtatca ctggtgacat caagaatate agg aggcatettt gttteetggt gecetectea aagttgetga caetttgggg aeg gtagaagtag ggetgeteet tttggagetg gagggaatag acctggagae agg cagteggget gtecaggtte taagcateae agettetgea ctgggetetg cagecagagg ateccagect cetecteet caaatgtcaa g</pre>	agagggg 120 gctgggg 180 ggaaggg 240 gttgagg 300
<210> 41 <211> 401 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(401) <223> n = A,T,C or G	·
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<210> 42 <211> 310	

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<212> DNA
      <213> Homo sapien
      <400> 42
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                                                                      120
tttggggtga atggatttct ttaataccaa taatattttt aattcccacc acagatggat
                                                                      180
ttgctgaata tgctaatgct gtgaatgaga aaacaatttt ggggtaggta tacccacaag
                                                                      240
taatctgatg acaaaataaa ccacagactg atgtcaaatg gacaaaaaac tgaaaatatg
                                                                      300
ctgtgagaaa
                                                                      310
      <210> 43
      <211> 401
      <212> DNA
      <213> Homo sapien
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                                                                       60
ctttcatgcc tctgatcatg tgcccaagcc aggagtgcca aaccaaccgc tcaggagggc
                                                                      120
ggctgtatct gcagacacgg ggctccagat tcatcaaatt ccaggagatg aagatgcaag
                                                                      180
aacatagtga tcaggtgcct gtgggaaata tccctcgtag tatcacggtg ctggtagaag
                                                                      240
gagagaacac aaggattgcc cagcctggag accacgtcag cgtcactggt attttcttgc
                                                                      300
caatcetgeg cactgggtte egacaggtgg tacagggttt acteteagaa acetacetgg
                                                                      360
aagcccatcg gattgtgaag atgaacaaga gtgaggatga t
                                                                      401
      <210> 44
      <211> 401
      <212> DNA
      <213> Homo sapien
      <400> 44
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                                                                        60
ttggcagatt aaatetttgc aaaatteeat atgtgetatt gaaaaatgaa ataaaacete
                                                                      120
agatgtctga attcttattt caaatacagt tatataatta ttttaaatta caatatacaa
                                                                      180
tttctgttaa atacaactgt taagggattc tgagaacaat tataagatta taataatata
                                                                      240
tacaaactaa ettetgaaat gacatgggtt gttteettee caceeteeta eeeteteaaa
                                                                      300
gagtttttgc atttgctgtt cctggttgca aaaggcaaaa gaaaatctaa aaatagtctg
                                                                      360
tgtgtgtcca cgacatgctc gctcctttga gaatctcaaa c
                                                                      401
      <210> 45
      <211> 401
      <212> DNA
      <213> Homo sapien
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      <221> misc_feature
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      <223> n = A, T, C or G
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gctacagtgg gaacaggctc aggactatct caagagattt tatctctatg actcagaaac
                                                                      120
aaaaaatgcc aacagtttag aagccaaact caaggagatg caaaaaattc tttggcctac
                                                                      180
ctatactgga atggtaaact cccgcgtcat anaaataatg caanaagccc agatgtggag
                                                                      240
tgccagatgt tgcagaatac tcactatttc caaatagccc aaaatggact tccaaagtgg
                                                                      300
tcacctacag gatcgtatca tatactcgag acttaccgca tattacagtg gatcgattag
                                                                      360
tgtcaaaggc tttaaacatg tggggcaaag agatcccct g
                                                                      401
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<210> 46
      <211> 401
      <212> DNA
     <213> Homo sapien
      <220>
      <221> misc feature
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     <223> n = A, T, C or G
      <400> 46
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                                                                       60
catgattcan agatactgcc ttctctctct ctgggatttt atgtgtttct gatagtgaat
                                                                      120
tgttgatgta tttgctactt tgcttctttt ctctttcaag acttgatcat tttatatgct
                                                                      180
gnttggagaa aaaaagaact tttggtagca aggaggtttc aagaaatgat tttggatttt
                                                                      240
ctgctgcgga atttctcggc acctacctgt agtatggggc acttggtttg gttgcagagt
                                                                      300
aagaaggtgg aagaatgagc tgtacttggt taagcagttg aaaccttttt tgagcaggat
                                                                      360
ctgtaaaagc ataattgaat ttgtttcacc cccgtggatt c
                                                                       401
      <210> 47
      <211> 401
      <212> DNA
      <213> Homo sapien
      <400> 47
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                                                                        60
gttctcagat ccagacaaat ggaggaaaag aacatttatg cttccgtttc agaaagccaa
                                                                      120
gtcgtagttt tggcccttcc tttctctaaa gtttattccc aaaaacaggt agcattcctg
                                                                      180
attgggcaga gaagaggata ttttcagccc acatctgctg caggtatgtc attttctccc
                                                                      240
atcttcactg tgactagtaa agatctcacc acttctcttt ggaatttcca actttgcttg
                                                                      300
tgattgaatg tcacttcgtg aatttgtatt atgtcagatc acttggcatt gctcttccat
                                                                      360
atgcatcaag ttgccaggca ctaaacccaa tgttcatgaa c
                                                                      401
      <210> 48
      <211> 430
     <212> DNA
     <213> Homo sapien
      <400> 48
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                                                                       60
                                                                      120
aggattttct gaagatgctt caatgaaaat catcatttcc tctttaqtca tcccaagtct
tggtttgaaa aacttgggca tggacttata cagacettga accaccactg acttatcatt
                                                                      180
gggtggcaga ccttgaaacc aagctctctg tgttacttct gaaagtgcat caattctgat
                                                                      240
ttggctaaga acagaagaca aatactggga tcgtgattct gtgttatact ctagccacag
                                                                      300
catagoagct totogaacgg tttottcott ttotacattt aaattgtcac tactgagaat
                                                                      360
atctatcagt aggtcatgtg acagacctgc cccggggccg gcccgctcga tgcttgccga
                                                                      420
atatcatggt
                                                                      430
     <210> 49
      <211> 57
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     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(57)
     <223> n = A, T, C or G
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```
<400> 49
ggtattaaca atatcangca ctcattcttc ccctcttatg aaanggatna attttta
                                                                      57
     <210> 50
     <211> 327
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
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     <223> n = A, T, C or G
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                                                                        60
ttaattgnnn tatgnntgnc cttctggtgg ntgtngaagc ttcatatnnt ntttggacat
                                                                       120
cattacacgt cttagctctt tnaagnacaa ctttaatgct atatgaattt tgccattttn
                                                                       180
gctaacactg gtatgctccn ngcatccacc atnccacntg gaattattta ttncnttcat
                                                                       240
attaatnttt tgtttaccaa atctnacttg acccgaacga aactttctgn gtattttang
                                                                       300
gccccccat tcttactttt caagect
                                                                       327
      <210> 51
      <211> 236
      <212> DNA
      <213> Homo sapien
      <400> .51
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                                                                        60
cttgttgaat tgcttgaaca tgcggcccac atcctgggca aactcctgtg gggagctgta
                                                                       120
                                                                       180
gggaggtgac aactteteet ggaggeggge aeggateagg gteagateea gggtgeeaee
gggctggtcc agggagaagg tggagtcgta gccagacctg cccgggcggc cgctcg
                                                                       236
      <210> 52
      <211> 291
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
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     <223> n = A, T, C \text{ or } G
     <400> 52
ctcacatcct gggtccggct gtagagctgc accatggtgc tgagcgcccc ctccagctcc
                                                                       60
ttgtagatgt aaaggacggc gaaggagctg tagtctgtgt ccacgatgcg cacgtccagg
                                                                       120
tagcccaagg ccgggactct gaagttgtcc ctcggagccc accttcangt actcgggcat
                                                                       180
ccacctggtt acageentte gneeteggna acteeatntg gaetttacag geegeectee
                                                                       240
tctgtgggcc tgatggncct tgcaggacat nggaacacgg gagctcnctt t
                                                                       291
      <210> 53
     <211> 95
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(95)
     <223> n = A, T, C or G
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<400> 53
gtctgtgcag tttctgacac ttgttgttga acatggntaa atacaatggg tatcgctgan
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cactaagttg tanaanttaa caaatgtgct gnttg
                                                                        95
      <210> 54
      <211> 66
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(66)
      <223> n = A, T, C or G
      <400> 54
cctnaatnat ntnaatggta tcaatnnccc tgaangangg gancggngga agccggnttt
                                                                        60
gtccgg
                                                                        66
      <210> 55
      <211> 265
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(265)
      <223> n = A, T, C or G
      <400> 55
atctttcttc tcagtgcctt ggccntgttg agtctatctg gtaacactgg agctgactcc
                                                                        60
ctgggaaqag aggccaaatg ttacaatgaa cttaatggat gcaccaagat atatgaccct
                                                                       120
                                                                       180
gtctgtggga ctgatggaaa tacttatccc aatgaatgcc gtgttatgtt tttgaaaatc
ggaaacgcca gacttctatc ctcattcaaa aatctgggcc ttnctgaaaa ccagggtttt
                                                                       240
naaaatccca ttcnggtcnc cggcg
                                                                       265
      <210> 56
      <211> 420
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(420)
      <223> n = A, T, C or G
      <400> 56
gageggeege cegggeaggt cetegeggtg acetgatggg atttcaaaac ettggttete
                                                                        60
agcaaggccc agatttttga atgangatag aagtctggcg tttccgattt tcaaaacata
                                                                       120
acacgcattc attgggataa gtatttccat cagtcccaca gacngggtca tatatcttgg
                                                                       180
gtgcatccat taagttcntt tgttaacatt tgggcctctc tttcccangg gaattcagct
                                                                       240
cccagttgtt taccaanatt naactccacc ggggccaaag gcncttgaaa aaaaaaanaa
                                                                       300
ttccttgttt accttccttg ggcttnaagt tctggcgtcc aaaagttcaa tttgaaaact
                                                                       360
gcaccgcact taccacgtct cttcnagaan cctggggaca cctcggccgc gaccacgcta
                                                                       420
      <210> 57
      <211> 170
      <212> DNA
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<213> Homo sapien	
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<210> 58 <211> 193 <212> DNA <213> Homo sapien	
<pre><400> 58 attttcagtg cgagagtcta ggcgattccc tggcttctcc acacattat cccaacataa ctccatgaag tgatgcacct gtgcagtaaa ctgcgccttc tgctgctcgg cggccaccag gcgctgcaac tccgcttcat cggcttcgcc cagctccgcc attgttcgcc acctgcccgg gcggccgctc gaa</pre>	60 120 180 193
<210> 59 <211> 229 <212> DNA <213> Homo sapien	
<pre><400> 59 cgcaactctc gagcatttat atacaatagc aaatcatcca gtgtgttgta cagtctataa tactccaaca gtctcccatc tgtattcaat ggcgccaccc aatacagtcc tttgtttgga tgctggggag agtaatccct accccaagca ccatatagat aagaaaaaccc tctccagttg agctgaacca cagacggttt gctgatacct gcccgggcgg ccgctcgaa</pre>	60 120 180 229
<210> 60 <211> 340 <212> DNA <213> Homo sapien	
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<210> 61 <211> 179 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(179) <223> n = A,T,C or G	
<400> 61 tttttgtgac ggacgnttgg agtacatgtc ccaggatcac atccagcagc tagagtggct gggacaagct ggcggnggcc aagcactgtt gaaacnatag gggtctgggn gnactcgggt tnaagtggtt ggtccgantn ttnataacct tgtcngaacc nancatctcg gttgncang	60 120 179

<210> 62

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<211> 78
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(78)
     <223> n = A, T, C or G
     <400> 62
agggcgttcg taacgggaat gccgaagcgt gggaaaaagg gagcggtggc nggaagacgg
                                                                    60
ggatgagctt angacaga
                                                                    78
     <210> 63
     <211> 410
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1) ... (410)
     <223> n = A, T, C or G
     <400> 63
cccagttact tggggaggct gaggcaggga gaatcetttg aacceggngg gtgggaggtt
                                                                    60
gcagtgagcc cgagatagca ccattgcact tccancatgg ggtggacaga gtgagactct
                                                                   120
180
tntcccattt caagtcctga aaatagagga tcagaaatgt tgaggaattc tttaggatag
                                                                   240
aaagggagat gggattttac ttatggggaa agaccgcaaa taaagactgn aacttaacca
                                                                   300
cattccccaa gtgnaaggtg ttacccaaga agtaggaacc cttttggctn ttaccttacc
                                                                   360
ttccngaaaa aaacttattn cttaaaatgg aaacccttaa agcccgggca
                                                                   410
     <210> 64
     <211> 199
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(199)
     <223> n = A, T, C or G
     <400> 64
cttgttctca aaaaggtcaa agggagcccg acgaggaata aatagcaatg ccctgaattc
caactgacet tetacagaaa agtgettgae tgecaagtgg tetteceagt cattagtgag
                                                                   120
getettgtag aatteteeat acteetettg ggngangnea tnagggtttn nggeecaaat
                                                                   180
aggntgggcc tngttaagt
                                                                   199
     <210> 65
     <211> 125
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(125)
     <223> n = A,T,C or G
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<pre><400> 65 agcggtacag ttctgtcctg gcatcatcat aactcagtag cttgctaagg acatgaaacc gggta</pre>				60 120 125
<210> 66 <211> 204 <212> DNA <213> Homo sapien				
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<210> 67 <211> 383 <212> DNA <213> Homo sapien				
<220> <221> misc_feature <222> (1)(383) <223> n = A,T,C or G				
<400> 67 tcagggcctc caggcagcca gttttgcagg cgctcccaag aacctgctcc tgcaggggga gggctggtct tnaggcttga agtccaggtt ggcagtgtan ccgacgatgg ggtatttggc ggcctccagt tccttggccg tganacccgt ggacatcttg gctacccctc tagtggagtc tcgtccataa aactcctttt cgg	acatcagaac agggctgcca tttgtacact antgtcatgg	tcgtccttga tcctcattga ttggtgaaaa gtgaggtctg	tgtcaaaatg gaattctccg cctnatccag caggatccaa	60 120 180 240 300 360 383
<210> 68 <211> 99 <212> DNA <213> Homo sapien				
<400> 68 tcacatctcc tttttttttt aacttttca ttagatttaa gtttctgcta cattgaccct		ttaaatagaa	ggctaaaggg	60 99
<210> 69 <211> 37 <212> DNA <213> Homo sapien				
<220> <221> misc_feature <222> (1)(37) <223> n = A,T,C or G				
<400> 69 gagaaggacn tacggncctg ntantanang	aatctcc			37
<210> 70				

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<211> 222
       <212> DNA
       <213> Homo sapien
       <220>
       <221> misc feature
       <222> (1) ... (222)
       <223> n = A, T, C or G
       <400> 70
gtgggtcatt tttgctgtca ccagcaacgt tgccacgacg aacatccttg acagacacat
                                                                          60
 tcttqacatt qaaqcccaca ttqtccccaq qaaqaqcttc actcaaaqct tcatqqcqca
                                                                         120
 tttcqacaga ttttacttcc gttqtaacqt tqactqqaqc aaaggtqacc accataccgg
                                                                         180
                                                                         222
 gtttgagaac acccantcac ctgccccggg cggccgctcg aa
       <210> 71
       <211> 428
       <212> DNA
       <213> Homo sapien
       <220>
       <221> misc feature
       <222> (1) ... (428)
       <223> n = A, T, C or G
  caggagtatt ttgtagaaaa gccagaagag cattagtaga tgtatggaaa tatacggtag
                                                                          60
  ggcacacgct gacagtactt ttcccaagcc acgccgtatt tcttcttaca gtggtactcg
                                                                         120
                                                                         180
  tcacgagctt ctcggtggac aagcaacatg gtgaaataaa ttatgtagaa ataaggcaga
  atgtggttaa aaccacatgg gagggaccac gccaaggcca tgatgagatc acccaagtaa
                                                                         240
                                                                         300
 ttggggtggc gaacaaagcc ccaccatcca gaaactagaa naatttttcc cgttgaaata
 tgaatggntt ttaaatgtgc aagctttgga tcactgggaa ttttcccgaa tgcctttttc
                                                                         360
  tganaattgc accttnggaa gantccttac cccaagnttc agaccattat ttnaaaagcn
                                                                         420
  ttggaact
                                                                         428
       <210> 72
       <211> 264
       <212> DNA
       <213> Homo sapien
       <220>
       <221> misc feature
       <222> (1)...(264)
       <223> n = A, T, C or G
       <400> 72
 gaataaagag cttactggaa tccagcaggg ttttctgccc aaggatttgc aagctgaagc
                                                                          60
                                                                         120
 tetetgcaaa ettgatagga gagtaaaaag ccacaataga gcagtttatg aagatettgg
 aggagattga cacacttgat cctgccagaa aatttcaaag acagtagatt gaaaaggaaa
                                                                         180
 ggctttggta aaaaaaggtt caggcattcc tagccgantg tgacacagtg gagcanaaca
                                                                         240
 tetgeangag actganegge tgea
                                                                         264
       <210> 73
       <211> 442
       <212> DNA
        <213> Homo sapien
       <220>
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<221> misc feature
      <222> (1)...(442)
      \langle 223 \rangle n = A, T, C or G
      <400> 73
                                                                        60
ggcgaatccg gcgggtatca gagccatcag aaccgccacc atgacggtgg gcaagagcag
caagatgctg cagcatattg attacaggat gaggtgcatc ctgcaggacg gccggatctt
                                                                       120
                                                                       180
cattggcacc ttcaaggctt ttgacaagca catgaatttg atcctctgtg actgtgatga
                                                                       240
gttcagaaag atcaagccaa aqaacttcaa acaagcagaa agggaagaga agcgagtcct
cggtctggng ctgctgccaa gqqaqaatct ggtctcaatg acngtagaag gaccttcttc
                                                                       300
caaagatact ggnattgctc gaqttccact tgctggaact tcccggggcc caaggatcgc
                                                                       360
                                                                       420
aaggettetg geaaaagaaa teeanaettn ggeegggace acetaaneea atteacacae
                                                                       442
tggcggccgt actagtggat cc
      <210> 74
      <211> 337
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(337)
      <223> n = A,T,C or G
      <400> 74
ggtagcagcg tctccagagc ctgatctggg gtcccagata cccaggcagc agcagccctg
                                                                        60
                                                                       120
gaggtaaagg gcaagcteee caatgtgagg ggagaeeeca tteetggtea gecaggettt
cagaggagat agcaggtcga gggagccaac gaagaagaga ctgccancag gggaaggact
                                                                       180
                                                                       240
gtcccgccaa ggacagaact gattcagggg ggtcaatgct cctctagaga agagccacac
agaactgggq gqtccaqqaa ccatqaanct tggctgtqgt ctaaggagcc aggaatctgg
                                                                       300
                                                                       337
acagtgttct gggtcatacc aggattctgg aattgta
      <210> 75
      <211> 588
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(588)
      <223> n = A, T, C or G
      <400> 75
catgatgagt tctgagctac ggaggaaccc tcatttcctc aaaagtaatt tatttttaca
                                                                        60
                                                                       120
gcttctggtt tcacatgaaa ttgtttgcgc tactgagact gttactacaa actttttaag
acatgaaaag gcgtaatgaa aaccatcccg tccccattcc tcctcctctc tgagggactg
                                                                       180
gagggaagec gtgcttctga ggaacaactc taattagtac acttgtgttt gtagatttac
                                                                       240
actttgtatt atgtattaac atggcgtgtt tatttttgta tttttctctg gttgggagta
                                                                       300
tgatatgaag gatcaagatc ctcaactcac acatgtagac aaacattagc tctttactct
                                                                       360
ttctcaaccc cttttatgat tttaataatt ctcacttaac taattttgta agcctgagat
                                                                       420
                                                                       480
caataagaaa tgttcaggag agangaaaga aaaaaaatat atgttcccca tttatattta
qaqaqaqacc cttantcttg cctgcaaaaa qtccaccttt catagtagta ngggccacat
                                                                       540
                                                                       588
attacattca gttgctatag gncagcactg aactgcatta cctgggca
      <210> 76
      <211> 196
      <212> DNA
      <213> Homo sapien
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<400> 76
geggtateae ageetggeee ceatgtaeta teggggggee caggetgeea tegtggteta
                                                                       60
tgacatcacc aacacagata catttgcacg ggccaagaac tgggtgaagg agctacagag
                                                                      120
graggreage recaarateg trattgrart rgraggtaar aaggragare tggaretger
                                                                      180
cgggcggccg ctcgaa
                                                                      196
     <210> 77
     <211> 458
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(458)
     <223> n = A, T, C or G
      <400> 77
agtagagatg gggtttcact gtgttaacca ggatggtctt gatctcctgg cctcgtgatc
                                                                       60
tgcccgcctc ggcctcccaa agtgttggga ttacaggcgt gaaccaccgc acccggccag
                                                                       120
aaatgttagt ttttccctat tctctccct ttttcctatt atatacttgg tcaaccagac
                                                                       180
agccatccta ccccanaatg gtaatgcctc ttcattcctc atatgaggga ataaaagaga
                                                                       240
aaaaagcttt tggaaaacat ccacttatct aatcatccca aatatgtaat caaaagtata
                                                                       300
caactcatgt gaagaataca ctggtaaaat gttantatag gccaaggtat cttgaattcc
                                                                       360
tatatagaaa gctggtaaat gcccttttgg ctggaaccgc catcttccnn taattcnccc
                                                                       420
aaaatgacca aacacaaagg gnaagangan aagccccc
                                                                       458
     <210> 78
     <211> 464
      <212> DNA
      <213> Homo sapien
     <220>
     <221> misc feature
      <222> (1)...(464)
     <223> n = A, T, C or G
     <400> 78
teegeaaatt teetgeegge aaggteeeag catttgaggg tgatgatgga ttetgtgtgt
                                                                       60
ttgagagcaa cgccattgcc tactatgtga gcaatgagga gctgcgggga agtactccag
                                                                      120
aggcagcagc ccaggtggtg cagtgggtga gctttgctga ttccgatata gtgccccag
                                                                      180
ccagtacctq gqtqttcccc accttqqqca tcatqcacca caacaaacaq qccactqaqa
                                                                      240
                                                                      300
atgcaaagga ggaagtgagg cgaattctgg ggctgctgga tgcttacttg aagacgagga
                                                                      360
cttttctggt gggcgaacga gtgacattgg ctgacatcac agttgtctgc accctgttgt
ggetetataa geaggnteta gaacettett ttegeangae etteggeegg accaegetta
                                                                      420
acccaaattc cacacattg cnggccgtac taanggaatc ccac
                                                                      464
     <210> 79
     <211> 380
     <212> DNA
      <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(380)
     <223> n = A,T,C or G
     <400> 79
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ctgtatgacc agtttttcca tctccttcac ttctaccttg atcagctcga agtccagttc
                                                                        60
agtqtaaqaa atqqtatcct tctccatqat qtcaattcqq acaqttaqqt ttaacaqttt
                                                                       120
cttttcatac acactaatta attggacata ttccctcact ttanaaagtt ctttctcaaa
                                                                      180
cttctganaa aaqaacatga actgtgaatt ccaagcgttc ccactctgtc cacgggaaaa
                                                                      240
ggtggtqtct ggcaqqqaaa caqaacactq qcaqqtccac qqtcatccac qqaqccqqtq
                                                                       300
aaattgggaa aacaactggg acacaqaacc tccgctgcct aagctgcggn tgggagcttg
                                                                       360
gaacccgacc tggaactgga
                                                                       380
     <210> 80
      <211> 360
      <212> DNA
     <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1) ... (360)
      <223> n = A, T, C or G
      <400> 80
togagoggeo geoogggoag gtootcagag agotgtttgt tnogettett caaaaactee
                                                                        60
tattetecae ttetgetaaa ggaetggatg acateaattg tgatageaat atttgtgggt
                                                                       120
gttctgtcan ncancatcgc actcctgaac aaagtagatg ttggattgga tcagtctctt
                                                                       180
tccacccaga tgactcctan atggtggatn atttcaaatc catcantcag tacctgcatg
                                                                       240
cgnggtccgc ctgtgtnctt tgtcctgcag gangggcnct actacacttc ttccnagggg
                                                                       300
canaacatgg tgtgcngcgg ccatgggctg qcaacantga ttcnctgctq cacccanatn
                                                                       360
      <210> 81
      <211> 440
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(440)
      <223> n = A, T, C or G
      <400> 81
acgtggtccg gcgagtctga cctgcagata tgaactcctt gggaaaccta cattctgcct
cagacatact gggggcaaat ggctttaaaa gtctggctca gggagccaag attacagaaa
                                                                       120
neegttgagt enceatacat ggacactgac aaaggaactg aagatateca aacaagceet
                                                                       180
cctggtcccg ngcctgcata aagatcggga ncggaacggt accngacgtc tgtggtcagg
                                                                       240
qqttqtqqaa aattqqaaaa aaccaqtcct qcccacattq acaqqqaaqc ctcaacqqaa
                                                                       300
attgaacaga tngtcttatc accagtctcc cctcctggat cntgtctcgg ctcnggggan
                                                                       360
tcagtgatca gtcctttcag gtggaagaag caaagaagat caacaanaag cngatcctct
                                                                       420
cacctgntac cagcatatgg
                                                                       440
      <210> 82
      <211> 264
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(264)
      <223> n = A, T, C or G
      <400> 82
agcgtggtcg cggccgangt cctgacattc ctgccttctt atattaatta tacnaataaa
```

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acaaaatagt gttgaagtgt tggagcggcg aaaatttttg gggggtggta tggacagaga 120 atgggcgatn ttctcanggc tgcttcaagt gggattgggg cngcgtggga tcatncagtg 180 gganagattn cnctqaccqq antctnttqq tanqqatnat cttqtqqqqa tqtqcaaqaq 240 ncattegtet eetgaatgan tggt 264 <210> 83 <211> 410 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1) ... (410) <223> n = A, T, C or G<400> 83 ancytggtcg cggccgangt ccacagttgt gggagagcca gccattgtgg gggcagctcc 60 acaggtaaga ctcgtgtcct gagcagcgca catcatccag gacaatgggt cctgagccct 120 gaccaaaccg ggcatttcct ggggctgaca tggcccagcc acagcccant tgcctgcaga 180 cgaaattggc atcattggtg teccagtant cateacacac ggtgccccag gaaceteegg 240 tatangaact ccacteggee tenanacetg tegeeteeat teeneageet cagggggeaa 300 actqqqattc aqatccttct gtgggtacag gtggtgatat cctgacaggc caactttctq 360 geetgagtgt tgactgange tgggcagaee tgeecgggeg geegetegaa 410 <210> 84 <211> 320 <212> DNA <213> Homo sapien <220> <221> misc feature <222> (1)...(320) <223> n = A, T, C or G<400> 84 tcgaacggcc gcccgggcag gtctgcccca ggtgtatcca tttgccqccq atctctatca 60 naaggagetg getaccetge nneqacqaan teetgaanat aateteacce neecagatet 120 ctctgtcgca atggagatgt cgtcatcggt ggncctgatc acaqqqcatt qqactcaqaq 180 anangthanc acagtgtnga agcgattgan nnagttcagt tgctggtctt acccqatntt 240 ggaaggaagg aaaacgtgtt angacgtatc tcgatgnant tgaccaaanc tgaangctnc 300 agggggcatc gcaaaganan 320 <210> 85 <211> 218 <212> DNA <213> Homo sapien <220> <221> misc feature <222> (1)...(218) <223> n = A, T, C or G<400> 85 togagoggeo geoogggeag gtotgetgeo egtgetggtg coattgeece atgtgaagte 60 actgtgccag cccagaacac tggtctcggg cccgagaaga ctcctttctc caggctntan 120 gtatcaccac taaaatctcc aggggcacca tnganatcct gggtgtccgc aatgttgcca 180 atgtctgtcc gcnnattggc tacccaactg ttgcatca 218

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<210> 86
     <211> 283
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1) ... (283)
     <223> n = A, T, C or G
     <400> 86
tcgacttctt gtgaaggttt tgganaaata tgtatcagtt cgttttattt gggtattcaa
                                                                        60
taatateett ggtgataatg etgaeteeat ggettetgae eecaaaaatt gaecetgetg
                                                                       120
ccactggttg tagccctgag attgattttt gtagccacga ttgtttcctc gtcctctgaa
                                                                       180
gtnctggttg tanttecete tgtngggeat tecetetgt tgtanttece tetgtttgan
                                                                       240
taactaccac ggccaggaaa aacaggggca cgaaggtatg gat
                                                                       283
      <210> 87
      <211> 179
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(179)
      <223> n = A, T, C or G
     <400> 87
agcgtggtcc cggccgatgt ctttctgtgt aagtgcataa cactccacat acttgacatc
                                                                        60
cttcangtca cgggccagct nttcagcant ctctggagtg ataggctact gtntgttctn
                                                                       120
ggcaagtgtc tcaanaatac aggggtcntc tctgagatga ntttcagtcc cgaaccctc
                                                                       179
     <210> 88
     <211> 512
      <212> DNA
      <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(512)
     <223> n = A, T, C or G
     <400> 88
tcgagcggcc gcccgggcag gtcctancan agaatcacca aatttatgga gagttaacag
                                                                       60
gggtttaaca ggaangaagt gcctttagta agttctcaag ccagangctg gaggcagcag
                                                                       120
ctaaatcaga ggacaggatc ctcagtgaaa gtgagccatt cggggtggca tgtcactcca
                                                                       180
ggaataagca caacttanaa acaaatgatt tcgtangata gcacagtgac attggtgcac
                                                                       240
ttgtgaacct gaggccactg tgtcaaactg tgcactggtt gtgaataggg aganccaaaa
                                                                       300
attatgtcct actgggtaat gagctttcaa tgggctcgat cctctcacnc tgaaagctct
                                                                       360
gtagagcagc tcagaaccac aaccactccc aacattgacc cttctggggg tactgtctgt
                                                                       420
ggcacccaca ggaaggagct ggagatecec attaggactg tecacccaca ettgaageca
                                                                       480
caaaactgca cctcggccgc gaccaccgct ta
                                                                       512
     <210> 89
     <211> 358
     <212> DNA
     <213> Homo sapien
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<220>
              <221> misc feature
              <222> (1)...(358)
              \langle 223 \rangle n = A,T,C or G
              <400> 89
                                                                                                                                                                            60
tegageggge egecegggea ggtetgeeag tecceatece agacattett tgeatetaag
                                                                                                                                                                          120
ctgangtctg aactgagtgg ggtqggctgg tgtttccatc ctcacaactc cagtgagccg
ggtgtggccg tggcctgcqt ctctctggcg gttagtgatg ttggcatcat ccaccttttt
                                                                                                                                                                          180
caaaacaaaa gcactggact gaaqaanaat cccnccctgt ntccacccag tccatggttt
                                                                                                                                                                          240
                                                                                                                                                                          300
ttaataaaag ggttatnnaa gttgancaag ncatcaccac acacaancct aagaacnttt
ttcatcnntc cccaaaacaa acccncaccc tgggaactcc gggcgcgaac cacgccta
                                                                                                                                                                          358
              <210> 90
              <211> 250
              <212> DNA
              <213> Homo sapien
              <220>
              <221> misc_feature
              <222> (1) ... (250)
              <223> n = A, T, C or G
cgagcggccg cccgggcagg tctggatggg gagacggact ggaactgcgg cttcccgtgg
                                                                                                                                                                             60
                                                                                                                                                                          120
cctgcacgca caaggctccc cacggccgcc gaccttcttc agattcgatc gtatgtgtac
gcacnaagag ccaaatattg acattcacaa cttcgtggga atnttacccc anaagactgc
                                                                                                                                                                          180
gaccccccga tcaggcgana gcctgagcat agaagaacac cgctgtgggc ttggcactgt
                                                                                                                                                                          240
                                                                                                                                                                          250
gggncccatc
              <210> 91
              <211> 133
              <212> DNA
              <213> Homo sapien
              <220>
              <221> misc feature
              <222> (1) ... (133)
              <223> n = A, T, C or G
              <400> 91
tcgagcggcc gnccgggcag gtcccgggtg gttgtttgcc gaaatgggca agttcntnaa
                                                                                                                                                                             60
ncctgggaag gtggtgcntg tnctggctgg acgctactcc ggacgcnaag ctgtcntcgt
                                                                                                                                                                          120
gangancatt gat
                                                                                                                                                                          133
              <210> 92
              <211> 232
              <212> DNA
              <213> Homo sapien
              <220>
              <221> misc feature
              <222> (1) ... (232)
              <223> n = A, T, C or G
aggraphic confidence of the co
                                                                                                                                                                             60
aqcatqqctg taggggcgat ctgaggtgcc atcatcaatg ttcttcacga tgacaagctt
                                                                                                                                                                          120
```

```
tgcgtccgga gtagcgtcca gccaggacaa gcaccacctt cccacgtntt cangaactng
                                                                      180
cccatttcgg cataaccacc cgggacctgc ccgggcggnc gctcgaaaag cc
                                                                       232
      <210> 93
     <211> 480
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (480)
     <223> n = A, T, C or G
     <400> 93
agcgtgggtc gcggccgang tctgtangct caccgccag agaagaccac tgtgagcatt
                                                                        60
ttgccgtata tcctgccctg ccatttgttc actttttaaa ctaaaatagg aacatccgac
                                                                       120
acacaccgtt tgcatcgtct tctcccttga tattttaagc attttcccat gtcgtgagtt
                                                                       180
tctcagaaac atgttttaa caattgtact atttagtcat ngtccattta ctataattta
                                                                       240
tctgaccatt tccctactgt taaaatactt aagacggttt ctgatttttc cactatttaa
                                                                       300
ataatgctgt gatgaatatc tttaaaatct tctgatttct tacttttttc ccccttagat
                                                                       360
gcctggaagt ggtattttga ggtgaaagag tttgttcatt ttgaanatat ttctgtctct
                                                                       420
ctctcgacct gatgtgtana cgctcacttc cagttagcag aaccacctta gtttgtgtct
                                                                       480
      <210> 94
      <211> 472
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(472)
      <223> n = A, T, C or G
     <400> 94
togagoggno gocogggoag ggtotgatgt cantoacaac ttgaagggat gocaatgatg
                                                                       60
taccaatcon atgtgaaatc tctcctctta tctcctatgc tgganaaggg attacaaagt
                                                                       120
tatgtggcng ataannaatt ccatgcacct ctantcatcg atgagaatgg agttcatgan
                                                                       180
ctggtgaacn atggtatctg aacccgatac cangttttgt ttgccacgat angantagct
                                                                       240
tttatttttg atagaccaac tgtgaaccta ccacacgtct tggacnactg anntctaact
                                                                       300
atconcaggg ttttattttg cttgttgaac tcttncagct nttgcaaact tcccaagate
                                                                       360
canatgactg antitcagat agcattitta tgattcccan ctcattgaag gtcttatnta
                                                                       420
tntcnttttt tccaaqccaa ggagaccatt ggacctcggc cgcgaccacc tn
                                                                       472
     <210> 95
     <211> 309
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(309)
     <223> n = A, T, C or G
     <400> 95
tcgagcggcc gcccgggcag agtgtcgagc cagcgtcgcc gcgatggtgt tgttggagag
                                                                       60
cgagcagttc ctgacggaac tgaccagact tttccanaag tgccggacgt cgggcancgt
                                                                      120
ctatatcacc ttgaagaant atgacggtcg aaccaaaccc attccaaaga aangtactgt
                                                                      180
gganggettt ganeeegeag acaacnagtg tetgttaaga actacegatn ggaaanaana
                                                                       240
```

```
anatcagcac tgtgggtgag ctccnaggga agttaataan tttcggatgg gcttattcna
                                                                       300
acctcctta
                                                                       309
      <210> 96
      <211> 371
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (371)
      <223> n = A, T, C or G
      <400> 96
togagoggco geologigoag gtocaccact cacctactco cogtototat agatttgcct
                                                                        60
gttctgggca gttctcagca atggaatcct actgtgtatc tttttgtgac tggttcttta
                                                                       120
actcagcatc acattiticaa ggttcatcca tgctgcagcc tggctccgta ctggtgacag
                                                                       180
tacttcattt ctctcccct tttgttcaga ccaaggtctc cctctgtccc caaggctaaa
                                                                       240
gtgcagttgg tgtgatcatg gctcactgca gcctcaaact cctggactca aacagtcctc
                                                                       300
ccatctcage ctcccaaagt gctgatntta taagttgcaa gccctgcacc cagcctgtat
                                                                       360
ctccagtttg t
                                                                       371
      <210> 97
      <211> 430
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1) ... (430)
      <223> n = A, T, C or G
      <400> 97
teganeggee geeeggéeag gtttnttttn tttntttttt nnnngntagt atttaaagan
                                                                        60
atttattaaa tcatcttatc accaaaatgg aaacatnttc caactagaaa catgcnacca
                                                                       120
tcatcttccc cagtccagtc ncaangtcca atattttnct tgcctctgca gataaaaagt
                                                                       180
tennattttt atacceacte ttacteecce ceaaaatttt aattengtee tneectaaaa
                                                                       240
ttncnccggg taacaantta ccaaaatggc naaccaatta ttttaaanaa aagttgcncn
                                                                       300
ttnaaaangg aaactttntg gcaanttanc ctcttttccc ttcccacccc ccantttaag
                                                                       360
gggaaaacaa tggcactttg ctcttgcttn aacccaaaat tgtcttccaa aaactattaa
                                                                       420
aaatgttnaa
                                                                       430
      <210> 98
      <211> 307
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(307)
      <223> n = A, T, C or G
      <400> 98
tenaacggcc gecenggenn gtetngenge acetgtgeet cancegtega tacetggteg
                                                                        60
attgggacan ggaanacaat ntggttttca gggaggccac anatttggag aaacggatga
                                                                       120
attotecttt atteegaant cageteettg gteteegtag anggtgatet tgaaattete
                                                                       180
ctgttttgaa aactttcttg aanaaacctt acctgctggt tgtatttggt ctcccactcg
                                                                       240
gacaagtact cgttatccnn ggtactctta atgtgcccac gtnaactccc cgggntggca
                                                                       300
```

```
actggaa
                                                                        307
      <210> 99
      <211> 207
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(207)
      \langle 223 \rangle n = A,T,C or G
      <400> 99
gtccnggacc gatgttgcna aganntttct tggtccanta ggttcnaaaa aatgataanc
                                                                         60
naggtntanc acgtgaagat ntntatanag tottantnaa aacnontaga totgnatgac
                                                                        120
gataantcga anacnggggg aggggntgag gngaggtggn gtganggaag anntgttgat
                                                                        180
aaaagannna gntgataaga anngagc
                                                                        207
      <210> 100
      <211> 200
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (200)
      <223> n = A,T,C or G
      <400> 100
acntnnacta gaantaacag ncnttctang aacactacca tctgtnttca catgaaatgc
                                                                         60
cacacacata naaactccaa catcaatttc attgcacaga ctgactgtaa ttaattttgt
                                                                        120
cacaggaatc tatggactga atctaatgcn nccccaaatg ttgttngttt gcaatntcaa
                                                                        180
acatnnttat tccancagat
                                                                        200
      <210> 101
      <211> 51
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(51)
      <223> n = A,T,C or G
      <400> 101
tcgagcggcc gcccgggcag gtctgaccag tgganaaatg cccagttatt g
                                                                         51
      <210> 102
      <211> 385
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(385)
      <223> n = A, T, C or G
      <400> 102
```

```
aacgtggtcg cggccgaagt ccatggtgct gggattaatc cactgtgacn gtgactctga.
                                                                        60
gttgagttgt ttttcaatct tctccaagcc tgtggactca tcctccacat ccttgggtag
                                                                       120
taggatgaac atgctgaaga tgctnatttt gaaaaggaac tctatgaatc ttacaattga
                                                                       180
atactqtcaa tqtttcccca tnacaqaacq tqqnccccca aqqttccatc atctqcactq
                                                                       240
ggtttgggtg ttctgtcttg gttgactctt gaaaagggac atttcttttt gttttcttga
                                                                       300
attcanggaa attttcttca tccactttgc ccacaaaagt taggcagcat ttaaccccca
                                                                       360
                                                                       385
anggattttg ggtctgggtc cttcc
      <210> 103
      <211> 189
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(189)
      \langle 223 \rangle n = A,T,C or G
      <400> 103
agcgtggtcg cggccgaagt ctgcagcctg ggactgaccg ggaagctctg attatttacc
                                                                        60
caccacaggt angttgtgtt ctgaatctca agttcacagg ttaaggctac agcatcctca
                                                                       120
tectecacgg ggttggantt gttgetggtg atgaanggtt tggggtgget etgeataact
                                                                       180
gttgatctc
                                                                       189
      <210> 104
      <211> 181
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(181)
      <223> n = A, T, C or G
      <400> 104
tegageggee geeegggeag gteeaggtet ceaceaange accaeegtgg gaagetggta
                                                                        60
attgatgccc accttgaagc cnntggggca ccatccncca actggatgct gcgcttggtt
                                                                       120
ttgatggtgg caatggcaca ttgactcttt tgggaaccac ttcaccacgg tacaacagge
                                                                       180
                                                                       181
      <210> 105
      <211> 327
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(327)
      <223> n = A, T, C or G
     <400> 105
tcgagcggcc gcccgggcag gtcttctgtg gagtctgcgt gggcatcgtg ggcagtgggg
                                                                        60
ctgccctggc cgatgctcan aaccccagcc tctttgtaaa gattctcatc gtgganatct
                                                                       120
ttggcagcgc cattggcctc tttggggtca tcqtcqcaat tcttcanacc tccanaatqa
                                                                       180
anatgggtga ctanataata tgtgtgggtn gggccgtgcc tcacttttat ttattgctgg
                                                                       240
ttttcctggg acagaactcg ggcgcgaaca cgcttanccg aattccaaca cactggcggg
                                                                       300
cottactagt ggatccgagc tcggtac
                                                                       327
```

```
<210> 106
      <211> 268
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1) ... (268)
      <223> n = A, T, C or G
      <400> 106
agegtggteg eggeegangt etggegtgtg ceacateggt eccacetege tttacaaaac
                                                                        60
agtoctgaac ttnatctaat aaaattattg tacacnacat ttacattaga aaaaganagc
                                                                       120
tgggtgtang aaaccgggcc tggtgttccc tttaagcgaa ngtggctcca cagttggggc
                                                                       180
atcgtcgctt cctcnaagca aaaacgccaa tgaaccccna aggqqqaaaa aqqaatqaaq
                                                                       240
gaactgnccn gggangnccg ctccgaaa
                                                                       268
      <210> 107
      <211> 353
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (353)
      <223> n = A, T, C or G
      <400> 107
tcgagcggcc gcccgggcag gtggccaggc catgttatgg gatctcaacg aaggcaaaca
                                                                        60
cctttacacn ctagatggtg gggacatcat caacgccctg tgcttcagcc ctaaccgcta
                                                                       120
ctggctgtgt gctgccgcag gccccagcat caagatctgg gatttanagg gaaagatcnt
                                                                       180
tgtnnatgaa ctgaancnta aattatcagt tccannacca ngcaaaaacc acccngtgca
                                                                       240
ctccctggcc tggtctgctg atgggacctc gggcgcgaac acgctnancc caattccanc
                                                                       300
acactgggcg gncgttacta ntggatccga actcnggtac caancttggc gtt
                                                                       353
      <210> 108
      <211> 360
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(360)
      <223> n = A, T, C or G
agcgtggtcg cggccgaagt cctggcctca catgaccctg ctccagcaac ttgaacagga
                                                                        60
naagcagcag ctacatcett aaggteegga aagttagatg aagatttgga teetgeattg
                                                                       120
nectgeetee cacetatete tecenaatta taaacageet eettgggaag cageagaatt
                                                                       180
taaaaaactct cccnctgccc tnttgaacta cacaccnacc qqqaaaacct ttttcanaat
                                                                       240
ggcacaaaaa tncnagggaa tgcatttcca tgaangaana aactgggtta cccaaaatta
                                                                       300
ttgggttggg gaaatccngg gggggttttn aaaaaagggc aanccnccaa anaaaaaac
                                                                       360
      <210> 109
      <211> 101
      <212> DNA
      <213> Homo sapien
```

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<220>
      <221> misc_feature
      <222> (1)...(101)
      <223> n = A, T, C \text{ or } G
      <400> 109
atcgtggtcn cggccgaagt cctgtgtcct ggatgggccg tgtgcancga atccgttggc
                                                                        60
gactcctaac taccaanaaa angactctcg gaagaaattt c
                                                                        101
      <210> 110
      <211> 300
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(300)
      <223> n = A, T, C or G
      <400> 110
ccanggaaac ccagagteac atgagatagg gtggctttcg ggacaggggg tcagangaat
                                                                        60
ggtacatgga tctcagcccc tgatggacac ggaacaggtg tggtcagaac tcccangatt
                                                                        120
ctgcatccan gatccagtct ctatagaagt tatggatcat tccttcattt cattccccc
                                                                        180
ttcatgaaaa aacttctgaa caagcctttt ttctcacttt ggggccctgt ttggcncaag
                                                                        240
qtnttnantt qqqqaaaaaa aaacaaatcc nttccnttan ccctccqtqq qqaatqacct
                                                                        300
      <210> 111
      <211> 366
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (366)
      <223> n = A, T, C or G
      <400> 111
cgagcggccg cccgggcagg tccttgtgtt gccatctgtt ancattgatt tctggaatgg
aacanctttc tcaaagtttg gtcttgctan tcatgaagtc atgtcagtgt cttaagtcac
                                                                        120
tgctgctcac ttccttaccc agggaatata ctgcataagt ttctgaacac ctgttttcan
                                                                        180
tattcactgt teeteteetg eccaaaattg gaagggacet catttaaaaa teaaatttga
                                                                        240
atcctgaaan aaaaacngga aatntttctc ttggaatttg gaatagaatt attcanttga
                                                                        300
ataacatgtt ttttcccctt gccttgctct tcncaanaac atctggacct cggccgcgac
                                                                        360
acctta
                                                                        366
      <210> 112
      <211> 405
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(405)
      <223> n = A, T, C or G
      <400> 112
ctgactncta aacttctaat tcnatcaana taactactct ccttccgtct tncagagtgt
                                                                        60
```

tcacaataaa tctgtgaatc tggcatacac agttgctgga aaattgttct tcctccacna

aaaggtcaat tgttcnccnc atgaaanaag tccaaaacge cggcggaatt attnccccgt tgggaangaa tggggctttt attgttttgt caatgggcce cctcgctcan aanntgcccc anccacactt ggcgggccgt tactanttgg	tattatgggg tttccccctt ggggccggcc	aacggaattt tcttggcatt gctccaaaac	tnaataaatt gattgggccg	180 240 300 360 405
<210> 113 <211> 401 <212> DNA <213> Homo sapien				
<pre><400> 113 ggatagaaga gtatatgggt ttggcaccac aggcgcagat tctgaactaa cttgtaaggc gaatggtaag gagagtttat aggttttagg ggctttaatc ctttcaaagc atgctgtggg gtgattaggt tttaatgaga tggtaagggg tagaggtatc ttatacttgt ggggttaagg ggaggctttg gattaggaat aaggggcggc</pre>	ttgtctggtt agcccatgct atgagatatt tgcatgatcc tgggggggat	ttaggacagg gtagcaggca ggcatttgag ggtccgccaa ataagaggga	taaaatgggg agtgataaca cggggtaagg ggaagggaag	60 120 180 240 300 360 401
<210> 114 <211> 401 <212> DNA <213> Homo sapien				
<220> <221> misc_feature <222> (1)(401) <223> n = A,T,C or G				
<pre><400> 114 angtccacag gangcangag gccaggctcc ggaagcagca catggggttg aagaactgac ccatggctgt ggtggcgggg aagacggaca aggtttcct ggcttctggg gctcatctgg atccagggtt cagagctact ttcttggggg gtngaggggg gacggggnaa gggncatgct accacgctaa ggcccgaatt ncagcacact</pre>	tccacttccc gggtgacttc ctctgattcc actactnggg tgtgacccag	aggactggtg tggaagacag ggctccttct aatcccgttc gtttcccacc	gagctggtca tgaagactga ccaggtcaag tcatctgggg	60 120 180 240 300 360 401
<210> 115 <211> 401 <212> DNA <213> Homo sapien				
<pre><400> 115 atccctgtaa gtctattaaa tgtaaataat ttggcagatt aaatctttgc aaaattccat agatgtctga attcttattt caaatacagt tttctgttaa atacaactgt taagggattc tacaaactaa cttctgaaat gacatgggtt gagtttttgc atttgctgtt cctggttgca tgtgtgtcca cgacatgctc gctcctttga <210> 116 <211> 301</pre>	atgtgctatt tatataatta tgagaacaat gtttccttcc aaaggcaaaa	gaaaaatgaa ttttaaatta tataagatta caccctccta gaaaatctaa	ataaaacctc caatatacaa taataatata ccctctcaaa	60 120 180 240 300 360 401
<212> DNA <213> Homo sapien				

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<220>
      <221> misc feature
      <222> (1) ... (301)
      \langle 223 \rangle n = A,T,C or G
      <400> 116
ngatttaatt gnnagcttct ttttaatgga atnnttggct aaaatgaatt gatgattatg
                                                                        60
aatatcccta ggaggagtta gcatggannn tgatcatttt cttngnactc ctttangaca
                                                                       120
nggaaacagg natcaqcatg anggtancan aaaccttatn accnangcgc acganctgac
                                                                       180
ttcttccaaa gagttgnggt tccgggcagc ggtcattgcc gtgcccattg ctggagggct
                                                                       240
gattctagtg ntgcttatta tgctggccct gaggatgctt ccaanatgaa aataagangc
                                                                       300
t
                                                                       301
      <210> 117
      <211> 383
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(383)
      <223> n = A, T, C or G
      <400> 117
aattgcaact ggacttttat tgggcagtta cnacaacnaa tgttttcana aaaatatttg
                                                                        60
gaaaaaatat accacttcat agctaagtct tacagagaan aggatttgct aataaaactt
                                                                       120
aagttttgaa aattaagatg enggtanage ttetgaaeta atgeecaeag etecaaggaa
                                                                       180
nacatgteet atttagttat teaaatacea gttgagggea ttgtgattaa geaaacaata
                                                                       240
tatttgttan aactttgntt ttaaattact gntncttgac attacttata aaggagnctc
                                                                       300
taactttcga tttctaaaac tatgtaatac aaaagtatan ntttccccat tttgataaaa
                                                                       360
gggccnanga tactgantag gaa
                                                                       383
      <210> 118
      <211> 301
      <212> DNA
      <213> Homo sapien
      <400> 118
ctgctagaat cactgccgct gtgctttcgt ggaaatgaca gttccttgtt ttttttgttt
                                                                        60
ctgtttttgt tttacattag tcattggacc acagccattc aggaactacc ccctgcccca
                                                                       120
caaaqaaatq aacaqttqta qqqaqaccca qcaqcacctt tcctccacac accttcattt
                                                                       180
tgaagttcgg gtttttgtgt taagttaatc tgtacattct gtttgccatt gttacttgta
                                                                       240
ctatacatct gtatatagtg tacggcaaaa gagtattaat ccactatctc tagtgcttga
                                                                       300
                                                                       301
      <210> 119
      <211> 401
      <212> DNA
      <213> Homo sapien
      <400> 119
taaggacatg gacccccggc tgattgcatg gaaaggaggg gcagtgttgg cttgtttgga
                                                                        60
tacaacacag gaactgtgga tttatcagcg agagtggcag cgctttggtg tccgcatgtt
                                                                       120
acgagagcgg gctgcgtttg tgtggtgaat ggggaggaaa tgtcactgcc gaagaccaaa
                                                                       180
aacaagcttc ttggtataaa agactcttac agaatatgtg tattgtaatt tattgatctg
                                                                       240
gatgcttaag tgtcatggac agtaaatgaa tttgaacttt atgtttgagg acatgacatt
                                                                       300
gggtttgaaa atataaactg cttttgagca gtttaagtca gggcatttga gaataaaata
                                                                       360
ggaactttct cttcagtttg taaaactctc ttgccctctc t
                                                                       401
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PCT/US00/35596

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<210> 137 <211> 269 <212> DNA <213> Homo sapien	
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<210> 138 <211> 452 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(452) <223> n = A,T,C or G	
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<211> 474 <212> DNA <213> Homo sapien <400> 139 tgtgcctcat tgaggttaca attgaaacag atgtgagcac ctgagagact ttccctgatt 60 atattcctcc acaaaccact gtaccatatt accttattt atcttcttga aattcttatt 120 cattggcttg tttgttgtct ctttgcatta gatatatgta agctccttgg cataaatttg 180 acattggtag gggactgaca ttctaacctg gcccaggccc taggagagag ataactccac 240 aaagcagcac atactatctt aggttagcag ggagctaact caccatgtag cagatgaaaa 300 aaaccaaacc cagcactgtg cataaatacc acttgccaag aagtcaggtc ctcggcaacc 360 qagaatcaac ctcaqcacaa acqcaqqtqq ctqqqctctq ttccccctta qccaccacct 420 cagectetee ceteceetge eccaaqtqce caaqagettg getetetgtg ettt 474 <210> 140 <211> 487 <212> DNA <213> Homo sapien <400> 140 ettecetgee tegtgtteet gagaaaegga ttaatageee tttateeeee tgeaeeetee 60 tgcaggggat ggcactttga gccctctgga gccctcccct tgctgagcct tactctcttc 120 agactttctg aatgtacagt gccgttggtt gggatttggg gactggaagg gaccaaggac 180 actgacccca agctgtcctg cctagcgtcc agcgtcttct aggagggtgg ggtctgcctg 240 tectggtgtg gttggtttgg ceetqtttge tgtgactace ecceeecte eccqaacega 300 gggacggctg cctttgtctc tgcctcagat gccacctgcc ccgcccatgc tccccatcag 360 cagcatecag actiticagga agggeaggge cagecagtee agaacegeat eceteageag 420 ggactgataa gccatctctc ggagggcccc ctaataccca agtggagtct ggttcacacc 480 ctggggg 487 <210> 141 <211> 248 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1) ... (248) <223> n = A, T, C or G<400> 141 ttaaagatgg ggaaatgagg cctgnaaata gaaaagattt gcctagagtc acacacactg 60 tcaggtcagg tagagtcaaa atcaggcacc ccgactcaca gactgcttca cattgccatc 120 agagattgtc ctgcaacaat attatgttta gttctactgc agaatgataa ctggatctta 180 ccccctttgc ctgatctggc cacaaacttg tttttcaggt ctttccatta ggctctcttc 240 agctaatt 248 <210> 142 <211> 173 <212> DNA <213> Homo sapien <400> 142 tactaagatt gtccaagcct ccctcttaaa actttctttc cctttagagg aatcattact 60 togtattaaa agtttotact toottgtaga atatotacat coaatgggco atggcacaaa 120 atttaagtct agaaagaatc ttaaaggctc atcttatagt aaccagaggc agg 173

<210> 143

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<211> 511
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      <221> misc feature
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      <223> n = A, T, C or G
      <400> 143
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ttcagggcag agggaatgag qcaacccagt qgcagccccg ctgggccccg tggctcctgc
                                                                       120
tctcctattg gacgtagagg caggggagag acttctctat acaaatattc tcatcacaga
                                                                       180
agggatgate cttgctgctc tgccgtaggg tttttgatgc tgagctatgc tgcacatgac
                                                                       240
gttaacctaa agaacttgga ctgagctttt aaaaaaggac agcaaacaat tttataatcc
                                                                       300
ttaaagtgta atagacggtt acactagtgc agggtattgg ggaggctctt tgggtgtgga
                                                                       360
ggctgtcact tgtatttatt gtgactctaa atctttgata gtaaaacaaa tgtaaaaaga
                                                                       420
aatgtttgcc accagatggg aatagaagtt ccaataagca ggctggaatg ggtggctata
                                                                       480
cgttgtatca cgaggaagtt ttagactctg a
                                                                       511
      <210> 144
      <211> 190
      <212> DNA
      <213> Homo sapien
      <400> 144
cattettetg teacatgeea atteagttgt caateceatt gtetatgett accggaaceg
                                                                        60
agacttccgc tacacttttc acaaaattat ctccaggtat cttctctgcc aagcagatgt
                                                                       120
caagagtggg aatggtcagg ctggggtaca gcctgctctc ggtgtgggcc tatgatctag
                                                                       180
gctctcgcct
                                                                       190
      <210> 145
      <211> 169
      <212> DNA
      <213> Homo sapien
      <400> 145
gatgtggtta tctcctcaga tggccagttt gccctctcag gctcctggga tggaaccctg
cgcctctggg atctcacaac gggcaccacc acgaggcgat ttgtgggcca taccaaggat
                                                                       120
gtgctgagtg tggccttctc ctctgacaac cggcagattg tctctggat
                                                                       169
      <210> 146
      <211> 511
      <212> DNA
      <213> Homo sapien
      <400> 146
atctagagaa gatttgggaa acacatgata gctatggtta aatacttaac agggcaatca
                                                                        60
cagggaagat gactagattt cctaacatcc atgagtgaaa tttatagaag tatactctct
                                                                       120
gacttgatat aaaggaagat tttaaaaaac atgactgttc aggagtgttc aagtagggtc
                                                                       180
agatgaccag tgattgggaa tacttcgtaa gcaggagcaa gtaagatctg agccactgtt
                                                                       240
ctatcggtag ggtgtctgtg gtattccttg gtcaaagaag tactctaagc aacttcagtc
                                                                       300
tcacgaatta ctatcaccct cgtgggcata catgatggtt accctaaaga ggaagtttca
                                                                       360
gaaggcagta atattggatc ctggaatagt cagacaggag ccttcatgca gatacccttt
                                                                       420
tcagttctcc atacacccat tcacaagtgg tcacaaaaac acccagtacc tttacttggc
                                                                       480
tttacccact taacaatatg ctcaatatga g
                                                                       511
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<210> 147

<213> Homo sapien

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<211> 421
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(421)
      <223> n = A, T, C or G
      <400> 147
gaccagttga gttcttcctg gctattgtat aatccacagc cacactgtga aagcaaatct
                                                                        60
ggccagttag caacacaggg agaatctgcc tgaactgacc aaaggtqtcc atacttcatg
                                                                       120
tcagtgagaa tttcacctcc atcatgttct aaagagccaa caacagattc tagggcactg
                                                                       180
caaaatgett cagcaattaa ttgaagttet gtttgagtac attcatcatc tttgagaatg
                                                                       240
ctttctgggt cgttgtgagt cttgtgtctg atatatgcag ccaaatgagt ttcagtacag
                                                                       300
ccacctccca acaaagccca tggttccttg agtgttaact gcaggacatg cagtgccgtc
                                                                       360
                                                                       420
tgacacgtga gcttcagctc atcccangca gtgtcatttc tgttgcagag aagccaagct
                                                                       421
g
      <210> 148
      <211> 237
      <212> DNA
      <213> Homo sapien
      <400> 148
acacaccact gttggccttc catctgggtt aagtcaactg tgagtagaaa ccgaagataa
                                                                        60
cagttttgta ttcataatgg ccttttcata ctccaagtac ttttgagcac agagcctctt
                                                                       120
gettetgace tggcaettgg aacacagata tatatatett ttgttetgte cetgggaaac
                                                                       180
tgatatttgt gtaagacaac caccagatat tttctctaat aaaatcttct aaaatta
                                                                       237
      <210> 149
      <211> 168
      <212> DNA
      <213> Homo sapien
agagaaagtt aaagtgcaat aatgtttgaa gacaataagt ggtggtqtat cttgtttcta
                                                                        60
ataagataaa cttttttgtc tttgctttat cttattaggg agttgtatgt cagtgtataa
                                                                       120
aacatactgt gtggtataac aggcttaata aattctttaa aaggagag
                                                                       168
      <210> 150
      <211> 68
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(68)
      <223> n = A, T, C or G
      <400> 150
ggtggggttt ggcagagatg antttaaqtg ctqtqgccaq aaqcqqqqqq gqggtttgqt
                                                                        60
ggaaattt
                                                                        68
      <210> 151
      <211> 421
      <212> DNA
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aggtgacacg tattcgggat gaaagtataa tagtcattcc ttcaaccctt gcatttatgg
                                                                       60
actotggaaa togaagatoo acagtgagta aagatgttog tocaaagaca aaaaatagaa
                                                                      120
acagctcaac aaaqcqaqaq acaaaaaaac aaaatqqcac tqtqqctctq cctttqaaqt
                                                                      180
ctgggctcca gcagagggct qatcttccca caggagacga gacggcctat gacactctcc
                                                                      240
agaactgttq tcaqtqccqa attttacttc ccttqcccat tctaaatqaq caccaqqaqa
                                                                      300
agtgccagag gttagctcac caaaagaaac tccagtgggg ctggtgagat ggctcagcgg
                                                                      360
gtaagagcac ccgactgctc ttccgaaggt ccggagttca aatcccagca accacatggt
                                                                      420
                                                                       421
     <210> 152
     <211> 507
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1) ... (507)
     <223> n = A, T, C or G
     <400> 152
gaatteggea enagetegtg eegeeagggt nggteenttt tttgeteege etegeeanga
                                                                       60
cttcctacag ctatcgccag tcgtcggcca cqtcntcctt cngaggcctg ggcggcgct
                                                                       120
ccgtgcgttn tgggccgggg gtcgcctttc nctcncccag cattcacqqq ggctccggcq
                                                                       180
geogeggegt atcogtgtee teegeceqet ntgtqteete qteeteeten qqqqeetaeq
                                                                       240
gctngctgct acngcggctt cctgaccgct tccnacqggc tgctgqcngq caacqaqaaq
                                                                       300
ctaaccatgc agaacctnaa cnaccgcctg gcctcctacc tgnacaaggt gcgcnccctg
                                                                       360
taggeggeea aeggenaget agaggtgaag ateenetaet gggtaeeaga ageagggee
                                                                       420
tgggccctgc ccgactacag ccactnctnc acnaccatgc agtacctgcn ggganaagat
                                                                       480
tntngggngc caccatngag aactgca
                                                                       507
     <210> 153
      <211> 513
      <212> DNA
      <213> Homo sapien
      <400> 153
gaattoggoa ogaggtggot cagatgtoca otactgggag tatggtogaa ttgggaattt
                                                                        60
tattgtgaaa aagcccatgg tgctgggaca tgaagcttcg ggaacagtcg aaaaagtggg
                                                                       120
atcateggta aageacetaa aaceaggtga tegtgttgee ategageetg gtgeteeeeg
                                                                       180
agaaaatgat gaattotgca agatgggccg atacaatctg teacetteca tettettetg
                                                                       240
tgccgcgccc cccgatgacg ggaacctctg ccggttctat aagcacaatg cagccttttg
                                                                       300
ttacaagctt cctgacaatg tcacctttga ggaaggcgcc ctgatcgagc cactttctgt
                                                                       360
ggggatccat gcctgcagga gaggcggagt taccctggga cacaaggtcc ttgtgtgtgg
                                                                       420
agctgggcca atcgggatgg tcactttgct cgtggccaaa gcaatgggag cagctcaagt
                                                                       480
agtggtgact gatctgtctg ctacccgatt gtc
                                                                      513
      <210> 154
     <211> 507
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1) ... (507)
     <223> n = A, T, C or G
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<213> Homo sapien

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<400> 154
ggcacgagct cgtgccgaat tcggcncgag cagacacaat ggtaagaatg gtgcctgtcc
                                                                        60
tgctgtctct gctgctgctt ctgggtcctg ctgtccccca ggagaaccaa gatggtcgtt
                                                                       120
actetetgae etatatetae actgggetgt ceaageatgt tgaagaegte eeegegttte
                                                                       180
aggcccttgg ctcactcaat gacctccagt tctttagata caacaqtaaa gacaqgaaqt
                                                                       240
ctcagcccat gggactctgg agacaggtgg aaggaatgga ggattggaag caggacagcc
                                                                       300
aacttcagaa ggccagggag gacatcttta tggagaccct gaaagacatc gtggagtatt
                                                                       360
acaacgacag taacgggtct cacgtattgc agggaaggtt tggttgtgag atcgagaata
                                                                       420
acagaagcag cggagcattc tggaaatatt actatgatgg aaaggactac attgaattca
                                                                       480
acaaagaaat cccagcctgg gtcccct
                                                                       50.7
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      <211> 507
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      <213> Homo sapien
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      <221> misc_feature
      <222> (1) ... (507)
      <223> n = A, T, C or G
      <400> 155
ggcacgagga gacctaaggg ctgagtntcg ggaacaggag aaagctctgt tggccctcca
                                                                        60
gcagcagtgt gctgagcagg cacaggagca tgaggtggag accagggccc tgcaggacag
                                                                       120
ctggctgcag gcccaggcag tgctcaagga acgggaccag gagctggaag ctctgcgggc
                                                                       180
agaaagtcag tcctcccggc atcaggagga ggctgcccgg gcccgggctg aggctctgca
                                                                       240
ggaggccctt ggcaaggctc atgctgccct gcaggggaaa gagcagcatc tcctcgagca
                                                                       300
ggcagaattg agccgcagtc tggaggccag cactgcaacc ctgcaagcct ccctggatgc
                                                                       360
ctgccaggca cacagtcggc agctggagga ggctctgagg atacaagaag gtgagatcca
                                                                       420
ggaccaggat ctccgatacc aggaggatgt gcagcagctg cagcaggcac ttgcccagag
                                                                       480
ggatgaagag ctgagacatc agcagga
                                                                       507
      <210> 156
      <211> 509
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(509)
      <223> n = A, T, C \text{ or } G
      <400> 156
ggcacgagga cagagagaac cctgtngaaa gagcgttacc aggaggtcct ggacaaacag
                                                                        60
aggcaagtgg agaatcagct ccaagtgcaa ttaaagcagc ttcagcaaag gagagaagag
                                                                       120
gaaatgaaga atcaccagga gatattaaag gctattcagg atgtgacaat aaagcgggaa
                                                                       180
gaaacaaaga agaagataga gaaagagaag aaggagtttt tgcagaagga gcaggatctg
                                                                       240
aaagctgaaa ttgagaagct ttgtgagaag ggcagaagag aggtgtggga aatggaactg
                                                                       300
gatagactca agaatcagga tggcgaaata aataggaaca ttatgqaaga gactgaacgg
                                                                       360
gcctggaagg cagagatctt atcactagag agccggaaag agttactggt actgaaacta
                                                                       420
gaagaagcag aaaaagaggc agaattgcac cttacttacc tcaagtcaac tcccccaaca
                                                                       480
ctggagacag ttcgttccaa acaggagtg
                                                                       509
      <210> 157
      <211> 507
      <212> DNA
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<400> 157
ggcacgaggg cagccctcct accggcgcac gtggtgccgc cgctgctgcc tcccgctcgc
                                                                        60
cctgaaccca gtgcctgcag ccatggctcc cggccagctc gccttattta gtgtctctga
                                                                      120
caaaaccggc cttqtqqaat ttgcaagaaa cctgaccgct cttggtttga atctggtcgc
                                                                      180
ttccggaggg actgcaaaag ctctcaggga tgctggtctg gcagtcagag atgtctctqa
                                                                       240
qttqacqqqa tttcctqaaa tqttqqqqqq acqtqtqaaa actttqcatc ctqcaqtcca
                                                                       300
tgctggaatc ctagctcgta atattccaga agataatgct gacatggcca gacttgattt
                                                                       360
caatcttata agagttgttg cctgcaatct ctatcccttt gtaaagacag tggcttctcc
                                                                       420
aggtgtaagt gttgaggagg ctgtggagca aattgacatt ggtggagtaa ccttactgag
                                                                       480
agctgcagcc aaaaaccacg ctcgagt
                                                                       507
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      <211> 507
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      <223> n = A, T, C or G
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                                                                        60
tacaaaaccc acattgatgt cattcattat cggaaaacgg atgcaaaacg tctgcatggc
                                                                       120
cttqatqaag aagcagaaca qaaacttttt tcaqagaaac qtqtggaatt gcttaaggaa
                                                                       180
ctttccagga aaccagacat ttatgagagg cttgcttcag ccttggctcc aagcatttat
                                                                       240
gaacatgaag atataaagaa gggaattttg cttcagctct ttggcgggac aaggaaggat
                                                                       300
tttagtcaca ctggaagggg caaatttcgg gctgagatca acatcttgct gtgtggcgac
                                                                       360
cctggtacca gcaagtccca gctgctgcag tacgtgtaca acctcgtccc caggggccag
                                                                       420
tacacgtntg ggaagggctc cagtgcannt ggcctnactg cntacgtaat gaaagaccct
                                                                       480
gagacaaggn anctggnnct gnnacag
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      <221> misc feature
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      <223> n = A, T, C or G
      <400> 159
ggcacnanaa accaggatta tggtnnggat ccaaagattg ctaatgcaat aatgaaggca
                                                                        60
gcagatgagg tagctgaagg taaattaaat gatcattttc ctctcgtggt atggcagact
                                                                       120
ggatcaggaa ctcagacaaa tatgaatgta aatgaagtca ttagcaatag agcaattgaa
                                                                       180
atgttaggag gtgaacttgg cagcaagata cctgtgcatc ccaacgatca tgttaataaa
                                                                       240
agccagaget caaatgatac ttttcccaca gcaatgcaca ttgctgctgc aatagaagtt
                                                                       300
catgaagtac tgttaccagg actacagaag ttacatgatg ctcttgatgc aaaatccaaa
                                                                       360
qaqtttqcac agatcatcaa gattqqacqt actcatactc aqqatqctqt tccacttact
                                                                       420
cttgggcagg aatttagtgg ttatgttcaa caagtaaaat atgcaatgac aagaataaaa
                                                                       480
gctgccatgc caagaatcta tgagctcg
                                                                       508
      <210> 160
      <211> 508
      <212> DNA
      <213> Homo sapien
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<220>
      <221> misc feature
      <222> (1) ... (508)
      <223> n = A, T, C or G
      <400> 160
ggcacgagct tggagcaaag tcatctnaag gaattagagg acacacttca ggttaggcac
                                                                       60
atacaagagt ttgagaaggt tatgacagac cacagagttt ctttggagga attaaaaaaag
                                                                       120
gaaaaccaac aaataattaa tcaaatacaa gaatctcatg ctgaaattat ccaggaaaaa
                                                                       180
gaaaaacagt tacaggaatt aaaactcaag gtttctgatt tgtcagacac gagatgcaag
                                                                       240
ttagaggttg aacttgcgtt gaaggaagca gaaactgatg aaataaaaat tttgctggaa
                                                                       300
gaaagcagag cccagcagaa ggagaccttg aaatctcttc ttgaacaaga gacagaaaat
                                                                       360
ttgagaacag aaattagtaa actcaaccaa aagattcagg ataataatga aaattatcag
                                                                       420
gtgggcttag cagagctaag aactttaatg acaattgaaa aagatcagtg tatttccgag
                                                                       480
ttaattagta gacatgaaga agaatcta
                                                                       508
      <210> 161
      <211> 507
      <212> DNA
      <213> Homo sapien
      <400> 161
ggcacgageg ctaccggege etectetgeg gccactgage eggageegge etgageageg
                                                                       60
                                                                       120
ctctcggttg cagtacccac tggaaggact taggcgctcg cgtggacacc gcaagcccct
cagtagcctc ggcccaagag gcctgctttc cactcgctag ccccgccggg ggtccgtgtc
                                                                       180
etgteteggt ggeeggaeee gggeeegage eegageagta geeggegeea tgteggtggt
                                                                       240
gggcatagac ctgggcttcc agagctgcta cgtcgctgtg gcccgcgccg gcggcatcga
                                                                       300
gactateget aatgagtata gegacegetg caegeegget tgeatttett ttggteetaa
                                                                       360
gaatcgttca attggagcag cagctaaaag ccaggtaatt tctaatgcaa agaacacagt
                                                                       420
ccaaggattt aaaagattcc atggccgagc attctctgat ccatttgtgg aggcagaaaa
                                                                       480
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                                                                       120
gctctacggc tcacccaatg ctctggtgct actgattgct caagagaagg aaagaaacat
                                                                       180
atttgaccag cgtgccatag agaatgagct actggccagg aacatccatg tgatccgacg
                                                                       240
                                                                       300
aacatttgaa gatatctctg aaaaggggtc tctggaccaa gaccgaaggc tgtttgtgga
tggccaggaa attgctgtgg tttacttccg ggatggctac atgcctcgtc agtacagtct
                                                                       360
                                                                       420
acagaattgg gaagcacgtc tactgctgga gaggtcacat gctgccaagt gcccagacat
tgccacccag ctggctggga ctaagaaggt gcagcaggag ctaagcaggc cgggcatgct
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ggagatgttg ctccctggcc agcctga
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<211> 460

<212> DNA

<213> Homo sapien

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qqttqaqccc aqtqacacca tcqaqaatqt caaqqcaaaq atccaaqata aqqaaqqcat
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ccctcctqac caqcaqaqqc tqatctttqc tqqaaaacaq ctqqaagatq ggcgcaccct
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qtctqactac aacatccaqa aaqaqtccac cctqcacctq qtqctccqtc tcagaqqtqg
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gatgcaaatc ttcgtgaaga cactcactgg caagaccatc acccttgagg tggagcccag
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tgacaccatc gagaacgtca aagcaaagat ccaggacaag gaaggcattc ctcctgacca
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aaaggaagaa cagacccccc agaataagat tacagttgtt ggggttggtg ctgttggcat
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ggcctgtgcc atcagtatct taatgaagga cttggcagat gaacttgctc ttgttgatgt
                                                                      240
                                                                       300
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tatcacggct ggggcacgtc agcaagaggg agaaagccgt cttaatttgg tccagcgtaa
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tgatcaagca gattccacga atcctcggcc caggtttaaa taaggcagga aagttccctt
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tggagettta atttattaat geanacagna eetaacaaac eeacangtee taaactacea
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agcctgcatt aaaaatttcg gntggggcna cctcnnagca naacccaacc tccgagcaac
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tcatgctaag acttcaccag tcaaagctga actactatac tcaattgatc caataacttg
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accaacagan caagntacce tagggataac ancacaatee tattetagae ecettatnac
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caatangntt tacacctona tngnggaacc aggacatccg atggggcagn cgttattaaa
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ttggtcacca gngctgcttt taactctggn aaagtggata ttgttgtcat naatgacccc
                                                                        180
tncattgacc tnaactacat ggtttacatg ttccaatatg attccaccca tggcaaattc
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catngcaccg tnaaggctga gaacgggaag cttgtnatca atggaaatcc catcaccatc
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tttcangaac ganatccntn caaaaatcaa anttgggggc gatgcttggc cncttgaagt
                                                                        360
accepticaan gggaannnce ceactitgge centrittine aaneceaece caattiggen
                                                                        420
aaaaaaaaa gggnntttgg gggggggcct tttanntttt tttt
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                                                                        120
cancagttet cagacetgae agaqqtgett ttacacttee taactgatee anantangtg
                                                                        180
gaaatattnt tngttnatnt catntgaatn atccancncc aatcatanca nntttnattn
                                                                        240
cctcataanc nttgagaana gcnnccttnt gnttncanan ggtgctntga anangagtct
                                                                        300
cacangcaan caggtccaag cggatttnnt aactntgggt cttantgang agaaagncac
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ttacttttct gaaancngga agcagaatgc tcccaccctt gctcgatggg ccatacgtca
                                                                        420
agactctgat gattaaccag ctttanatat ggacnggaaa tt
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                                                                        120
ccctccccac agatggtgca tcccctggca naggctcctg ctcacagcct cacttctaac
                                                                        180
cttctggaac ccgcccacca ctgccaagct cactattgaa tccacgccgt tcaatqnntc
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53

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ccaaatgtgt atgtcgctgt gaagatctgg agaaacaaaa cagattactt catgatcaga
                                                                     300
togaaaaatt aagtgacaag gtogttgoot otgtgaagga aggtgtacaa qgtocaotga
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                                                                     120
aggaacaaaa aggaaacttg gaagggatca taaggcagca agaggctgat attcaaaatt
                                                                     180
ctaagttcag ttatgaacaa ctggagactg atcttcaggc ctccagagaa ctgaccagta
                                                                     240
ggctgcatga agaaataaat atgaaagagc aaaagattat aagcctgctt tctggcaagg
                                                                     300
aagaggcaat ccaagtagct attgctgaac tgcgtcagca acatgataaa gaaattaaag
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cagccatage tacgtgcgtt cgctacgagg attgagcgtc tccacccatc ttctgtgctt
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<210> 187 <211> 506 <212> DNA <213> Homo sapi	en				
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<210> 189					

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PCT/US00/35596

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Ser Ala Gln Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys 20 25 30

Arg Asn Ala Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe

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Leu Arg Asp Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu
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Arg Cys Pro Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly
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67

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gaaaccaatg ttgtaaattt gatgettata atgetttage caatgagage acaatgatat

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gattggctct gttctgctgc gggaactgaa gcctgtcctg tctcaggggt aacctgctta
                                                                      180
catctggact ttagaatctg gcacacaaca aaagtgcctg gcatccacta ctgctgcctt
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tcatttataa taatagccct tccatctggc agtgggggaa gaatacactc ttgacattct
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tgtctcctgc tttagaatgc tagtgtgtat ctatcatgta tgcaatactt tccccctttt
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      <211> 508
      <212> DNA
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                                                                      120
ttttccagca cccaacataa cttgtaagga ttccagtggc aatgaaacac attttactgg
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gaacgaagtt ggttttttca agcccatatc ttgccgaaat gtaaatggct attcctacaa
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agtggcagtc gcattgtctc tttttcttgg atggttggga gcagatcgat tttaccttgg
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ataccetget ttgggtttgt taaagttttg cactgtaggg ttttgtggaa ttgggagcet
                                                                      360
aattgatttc attcttattt caatgcagat tgttggacct tcagatggaa gtagttacat
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tatagattac tatggaacca gacttacaag actgagtatt actaatgaaa catttagaaa
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aacgcaatta tatccataaa tattttt
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      <212> DNA
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tggctacaca ctctcactac acacacagac cccacagtcc tatatgccac aaacacattt
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ccataacttg aaaatgagta ttttgcatat ctcagttcag gatatgtttt ttacaagtta
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atcctaaagt cataaagcaa gaagctattc atagtacaag attttatttg ctaagcttta
                                                                       300
caaattaaac totaaaaaat tattacaatg atactgaaag atattttatt ggcctttt
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tacageteet attgatagga catagtggaa gtgagetaca acgtagtacg tgtegtgtag
                                                                      180
                                                                      240
tacgatgtct agtgatgagt ttgctaatac aatgccagtc aggccaccta cggtgaaaag
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tgtggcgagt cagctaaata ctttgacgcc ggtggggata gcgatgatta tggtagcgga
                                                                      360
ggtgaaatat gctcgtgtgt ctacgtctat tcctactgta aatatatggt gtgctcacac
                                                                      420
gataaaccct aggaagccaa ttgatatcat agctcagacc atacctatgt atccaaatgg
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tt
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                                                                      120
tgcctgtgga ctgtttatgg tctgtccag
                                                                      149
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     <211> 391
     <212> DNA
     <213> Homo sapien
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ggcacaggag gatctctaaa gcagtagcca aacaccactt tgtaaaagga ctcttccatc
                                                                      180
agaqatqqqa aaaccattqq qqaqqactaq qacccatatq qqaattatta cctctcaqqq
                                                                      240
ccgagaggac agaatggata taatctgaat cctgttaaat tttctctaaa ctgtttctta
                                                                      300
gctgcactgt ttatggaaat accaggacca gtttatgttt gtggttttgg gaaaaattat
                                                                      360
ttgtgttggg ggaaatgttg tgggggtggg g
                                                                      391
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     <211> 374
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     <213> Homo sapien
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atcataaact cataaaaata attttaagat gccggaaaag gatactttga ttaaataaaa
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acactcatgg atatgtaaaa actgtcaaga ttaaaattta atagtttcat ttatttgtta
                                                                      180
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                                                                      360
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                                                                      374
aaaaaaaaa aaaa
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gtctttgtgt tatgatcaat gaagaagggc cggccgtttg gcgctatcct catttcccag
                                                                      120
ccgggtggca agaagctctg tgtgactttg tgttgtggtt tgggggagtt gtaaggtgat
                                                                      180
ggctgtgggg actgtgggtt
                                                                      200
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                                                                       120
atattaaaaa ggaaactaat tggaccattt tctatttgtc tattttatac aaaaaggcta
                                                                       180
cacaattgat acactctatt cagataacaa tcaattagag tgantatgaa ttactggcga
                                                                       240
                                                                       300
caccatcact caattettaa aaattagaaa ttgctgtagc agtattcact ataacttaac
actaccgaga gact
                                                                       314
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      <221> misc_feature
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ggctgcctac agtgctgctt cattgttagt gggtgaagaa ttcaagacca aaaagcctct
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totgatttat ocaatotttt tattatacat ttatottttg togttatata otggtgtgtg
                                                                       240
atccaagtta tacatgaata gaaaaagatg gtgttaaatt tgtgtgtagg ctgggaattc
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tngctaaagg aatggnaaaa aacctgtnnt tgnaaaattn acntgtccca aagnnaagga
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anctaaacgc ttttt
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ttaggcccac ctatgtaagt ctgttatact agctaatgtg cccatttgaa tagttcaagg
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gtcagctaat gctctgagct tcatggctcc agtataaaga acaaatttaa caaaattaag
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ctgttactgt agccgagtta cccttctgct ccacacatat gtagtgggat cttgcaggat
                                                                       300
ttccatagtg ccaattatca aaggeettga ctaettagea ttgetgtatt acagatgtge
                                                                       360
aaactgaggc actgaaaagt caaattt
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                                                                       120
acactetgae acatgetetg agaatactgg gactgetgtt teaaaaaaaa aggtteaaac
                                                                       180
ttattgtcac agcatcatca caaaatagag gatcaccatt ggtttgcttg gcttttcttt
                                                                       240
tttttttcc cccaagtgag gacctaactc caaataatac aatagaatat gcaaattatc
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<210> 244 <211> 397 <212> DNA <213> Homo sapien		·		
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tacageteet attgatagga catagtggaa gtgagetaca acgtagtacg tgtegtgtag
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tacgatgtct agtgatgagt ttgctaatac aatgccagtc aggccaccta cggtgaaaag
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aaagatgaat cctagggctc agagcactgc agcagatcat ttcatattgc ttccgtggag
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tgtggcgagt cagctaaata ctttgacgcc ggtqgggata gcgatgatta tggtagcgga
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ggtgaaatat gctcgtgtgt ctacgtctat tcctactgta aatatatggt gtgctcacac
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aagaatataa acttcagggt gaccgaaaaa tcagaatagg tgttggtata gaatggggtc
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tectneteeg eggggtenaa gaaggtggtg ttgangttge eggnetgtta ntagtatagn
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                                                                       673
gatgecanca get
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      <211> 149
      <212> DNA
      <213> Homo sapien
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      <211> 458
      <212> DNA
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      <221> misc feature
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ggcacaggag gatctctaaa gcagtagcca aacaccactt tgtaaaagga ctcttccatc
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agagatggga aaaccattgg ggaggactag gacccatatg ggaattatta cctctcaggg
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ccgagaggac agaatggata taatctgaat cctqttaaat tttctctaaa ctqtttctta
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gctgcactgt ttatqqaaat accaqqacca qtttatqttt qtqqttttqq qaaaaattat
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                                                                       420
ttgtgttggg ggaaatgttg tgggggtggg gttgagttgg gggtattttc taattttttt
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tgtacatttg gaacagtgac aataaatgan accccttt
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acactcatgg atatgtaaaa actgtcaaga ttaaaattta atagtttcat ttatttgtta
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tattatttga tgcaacagtt ttctgaaatg atatttcaaa ttgcatcaag aaattaaaat
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catctatctg agtagtcaaa atacaagtaa aggagagcaa ataaacaaca tttggaaaaa
                                                                       360
aaaaaaaaa aaaa
                                                                       374
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tgaaaaattg tctttcctta tcattggtgg gaggcttggt agcaaagtaa cattttttgg
                                                                    180
aaaagaggac agaaaaattg aactacagct tgagaacgta ttctttttt cctactttgt
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tattgcaaat tgaggaatca cttttaactg ttttaggtgt gtgtgtccag agtgagcaag
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gattatgttt ttggattgtc aaagaggatg cttagtctta aaataaaaat aaattt
                                                                    356
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     <212> DNA
     <213> Homo sapien
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cacaattgtt acactttatt cagattacaa ttaattagag tgattatgaa ttagtgttct
                                                                    240
acaccattac tcaattctta aaaattagaa attgctgtag cagtattcac tataacttaa
                                                                    300
                                                                    360
cactacgaga gacttaaaaa acagttactg caaaaaaaaa aaagagctac ttcaaagcaa
420
agggtttgat aaattccatc ttgtgatcca ttcttgtgca ttcttcactt cttgagtcac
                                                                    480
tccc
                                                                    484
     <210> 253
     <211> 379
     <212> DNA
     <213> Homo sapien
     <400> 253
aaaaagggct tagacttccc tttccatctg gaacatgtaa aattttgcag caacaggttt
                                                                     60
                                                                    120
totocoatto ottoagoaag aattocoago otacacacaa atttaacaco atottttot
                                                                    180
attcatgtat aacttggatc acaccagt atataacgac aaaagataaa tgtataataa
aaagattgga taaatcagaa gaggettttt ggtettgaat tetteaceca etaacaatga
                                                                    240
agcagcactq taggcagccc aaaacacacc aaacagtttt ataagtgtag acaccacttc
                                                                    300
aaatgatcca accaccaaaa gtacaggggc tattacaatg agaggaagta atgaatatcc
                                                                    360
                                                                    379
tataactcca aggacttgg
     <210> 254
     <211> 387
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(387)
     <223> n = A, T, C or G
     <400> 254
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                                                                     60
                                                                    120
aggeenttga taattggeae tatggaaate etgeaagate ceactacata tgtgtggage
agaagggtaa ctcggctaca gtaacagctt aattttgtta aatttgttct ttatactgga
                                                                    180
                                                                    240
qccatqaaqc tcagagcatt agctgaccct tgaactattc aaatgggcac attagctagt
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75

```
ataacagact tacataggtg ggcctaaagc aagctcctta actgagcaaa atttggggct
                                                                      300
tatgagaatg aaagggtgtg aaattgacta acagacaaat catacatctc agtttctcaa
                                                                       360
                                                                       387
ttctcatqta aatcaqaqaa tqccttt
      <210> 255
      <211> 225
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(225)
      <223> n = A, T, C or G
      <400> 255
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                                                                        60
agcacctttg ataaaatata cttttgtgaa caaaaattga gacatttaca ttttctccct
                                                                       120
atgtggtcgc tccagacttg ggaaactatt catgaatatt tatattgtat ggtaatatag
                                                                       180
ttattgcaca agttcaataa aaatctgctc tttgtatgac agaat
                                                                       225
      <210> 256
      <211> 544
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(544)
      <223> n = A, T, C or G
      <400> 256
ccttgcttaa agcccagaag tggtttaggc ntttggaaaa tctggttcac atcataaaga
acttgatttg aaatgttttc tatagaaaca agtgctaagt gtaccgtatt atacttgatg
                                                                       120
ttggtcattt ctcagtccta tttctcagtt ctattatttt agaacctagt cagttcttta
                                                                       180
agattataac tggtcctaca ttaaaataat gcttctcgat gtcagatttt acctgtttgc
                                                                       240
tgctgagaac atctctgcct aatttaccaa agccagacct tcagttcaac atgcttcctt
                                                                       300
agetttteat agttgtetga cattteeatg aaaacaaagg aaccaacttt gttttaacca
                                                                       360
                                                                       420
aactttgttt ggttacagtt ttcaggggag cgtttcttcc atgacacaca gcaacatccc
                                                                       480
aaagaaataa acaagtgtga caaanaaaaa aacaaaccta aatgctactg ttccaaagag
                                                                       540
caacttgatg gtttttttta atactgagtg caaaaggnca cccaaattcc tatgatgaaa
                                                                       544
tttt
      <210> 257
      <211> 420
      <212> DNA
      <213> Homo sapien
      <400> 257
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                                                                        60
agcaatttga taaaatatac ttttgtgaac aaaaattgag acatttacat tttctcccta
                                                                       120
tgtggtcgct ccagacttgg gaaactattc atgaatattt atattgtatg gtaatatagt
                                                                       180
tattgcacaa gttcaataaa aatctgctct ttgtatgaca gaatacattt gaaaacattg
                                                                       240
gttatattac caagactttg actagaatgt cgtatttgag gatataaacc cataggtaat
                                                                       300
aaacccacag gtactacaaa caaagtctga agtcagcctt ggtttggctt cctagtgtca
                                                                       360
attaaacttc taaaagttta atctgagatt ccttataaaa acttccagca aagcaacttt
                                                                       420
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<210> 258 <211> 736

<212> DNA

76

<212> DNA <213> Homo sapien <400> 258 60 aaacaaaatg ctaaacctaa aaacattgtt ctgtcagttc ccaaattaaa tctacttaga acaaaaacaa aaatttatag ctcggtcaca tactacttaa ataatattgt tcaggcatct 120 ctaaaatcct ccatgttttc aagtatggaa atagaactca aatattccac aatacagtac 180 taaacagatg gagtatttag gaaagacttt gttgtcatat ggcacaatat taatattttg 240 ttgcttcaat acgttttgaa ataaatatca gatttttgtt ttttttcct aaaagaccaa 300 aattataatc tacattaaga taattctgac tgtggttaag acttaagagt gtaaaataca 360 acatcaatat tttatcacaa aagtaaagct ggtaacaaat tataaaagga gccagtactc 420 tactgagaca ggctcggaga ttaaagctca tcatgataga aatagtcatc atggagctgt 480 ctgccataat ctgtggcttc actggtgaga aacaagtccg ggttttccag aatctcttct 540 tcagagaget ttttqtcacc attcaaatcc atttcatcaa ttagatgaag cgcctcctct 600 tqtqcaatqc cctqattatt agqtctaccc aagqtaacaq ctcttqggga tcaagcctqc 660 720 categttate tttgtcataa tcattcaceg aatetgtett teteacaagt ateccattet ggatcttcat ttgcag 736 <210> 259 <211> 437 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1) ... (437) <223> n = A, T, C or G<400> 259 aaaaccatac tgaaatcatt taccaaataa cnaagatctt aatctaaaag atagtgaata 60 catcatcatc atgaaatctg gttttatgtg ctctatgaag tacttggaga attgcttttt 120 180 tatttttctt ttgctttatt aggtcacaca aaacagaatg aattagcaga aaaatgtatg 240 ttataaaaca gcatttacta cttcaattta attttttta ctaacaattg tggacctttt tgatgacact tatgtatgtt tttaataaat tatgtactta ttagtactta atgagccctt 300 cctgcctcaa tataaaatta ctaaacttgg agaattacag attttattgt aggccctgat 360 420 gttagtcact ttggagaagc taaaaattttg gaaatgatgt aattcccact gtaatagcat 437 agggattttg gaagcag <210> 260 <211> 592 <212> DNA <213> Homo sapien <400> 260 tttttttttt qaaaaatata aaattttaat aaaqqctaca tctcttaatt acaataatta 60 ttgtaccaag taattttcct taaatgaact ctttataatg cataatttac agtataagta 120 gaacaaaatg tcatgacaaa agtcattgag tacaagactt gtaataaaaa ggcataaaat 180 atatttatac ataaacccct ttcaaaaaac aagggaaagc ttgagccctc aatatagggc 240 300 qacacacqqa qcqqqtqacc qtqcaqqtac aqqtactqta ctqatttaaa qtcaaqcact agagatagtg gattaatact cttttgccgt acactatata cagatgtata gtacaagtaa 360 420 caatggcaaa cagaatgtac agattaactt aacacaaaaa cccgaacatc aaaatgaagg tgtgtggagg aaaggtgctg ctgggtctcc ctacaactgt tcatttcttt gtggggcagg 480 gggtagttcc tgaatggctg tggtccaatg actaatgtaa aacaaaaaca gaaacaaaaa 540 aaacaaggaa ctgtcatttc cacgaaagca cagcggcagt gattctagca gg 592 <210> 261 <211> 450

PCT/US00/35596 WO 01/49716 77

<213> Homo sapien <400> 261 gtggcagggc ccagccccga accagacaag ggacccctca aggagcttca ttctagcatg 60 agaaaattga gaagtaaacc agaaagttac agaatgtctg aaggggacag tgtgggagaa 120 tccgtccatg ggaaaccttc ggtggtgtac agatttttca caagacttgg acagatttat 180 cagteetgge tagacaagte cacaccetae aeggetgtge gatgggtegt gacactggge 240 ctgagctttg tctacatgat tcgagtttac ctgctgcagg gttggtacat tgtgacctat 300 gccttgggga tctaccatct aaatcttttc atagcttttc tttctcccaa agtggatcct 360 tccttaatgg aagactcaga tgacggtcct tcgctaccca ccaaacagaa cgaggaattc 420 cgccccttca ttcgaaggct cccagagttt 450 <210> 262 <211> 239 <212> DNA <213> Homo sapien <220> <221> misc feature <222> (1)...(239) <223> n = A, T, C or G<400> 262 taactttgat gacaaaatct aaaattaaag anttagtctt aaaagcctat agtgacttgt 60 ttacttgcat aaataatatt ttcacttagt acaggctatt aatataagta atgagaattt 120 aagtattaac tcaaaaaaag atagaggctc caaacttttc taagaaatta atgcattttc 180 aaagtaataa tataatcaat ctgtaagtca aaagtaattt catattcatt gccaaattt 239 <210> 263 <211> 376 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1)...(376) <223> n = A, T, C or G<400> 263 aaaaaaaaaa aaaaaaaatt ccttgtngtt tnttagagga aaaaaagaaa aaccccaact 60 tttancactg atactacata ttgctctgtt aaagaatttt ctctgccaaa aaaaagaaaa 120 aacaaaaaaa cgcttaaagc tggagtttga cattctgctt tcagatgctg tctttttatt 180 agtgagtgat gatggtttgc taataatcaa taggtaataa ttttttgtaa tcccatcaag 240 tggctccata tgtttctgct ctctcgtgac tgtgttaatg tttaactgtt gtaccttaaa 300 gccgaaatca gtaactatgc atactgtaac caaggtattg ggcttacaga gttgtttgtt 360 gnataaagaa aatttt 376 <210> 264 <211> 207 <212> DNA <213> Homo sapien <400> 264 aaattagcat tccacaaata tacaggtaat ttaataatta ttgtgcatga atacatacac 60 aatgcttata tatacaaatt ccagtttgtt ttcatgtgct ggcaagggat ttgtatacaa 120 tcataagctg tgttcatatt ggtcccattg aatattcaca atacaaaagc acaaaagaac 180 cattgattta caaaaggaaa tctattt 207

<212> DNA

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<210> 265
     <211> 388
     <212> DNA
     <213> Homo sapien
      <220>
     <221> misc feature
     <222> (1) ... (388)
     <223> n = A, T, C or G
     <400> 265
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                                                                       60
aaagnccnct gaaactgctt ccactgcctg ttgtatagaa atgggtaaat tataaaggtg
                                                                       120
                                                                       180
attcaatttg gagctccttc cttttttata gcacttctaa gctgtgtgcg cgacacacac
cacagaggta ggaaggacca cctttaataa attatcttct taatcgcaga gaatttctga
                                                                       240
                                                                       300
agataaaact gacaaaatgc taaaccaagg ctttgatgag tcccaaagga ccacagatcc
                                                                       360
atoggotoct atttgaagaa ttoatococt gtagtgttot agootttgta gggcactgga
                                                                       388
ttacaagatc caccagggct ctgaacaa
     <210> 266
      <211> 616
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(616)
     <223> n = A, T, C or G
     <400> 266
aaatacagag tcaaaagatg atttataaaa tntaaaacat tttctgcttg gccgtatttg
                                                                       60
aagacaaget gaatacatat etatgttetg aataagteea etatggatat atataggaag
                                                                       120
agatatacat atatccatcc acagatacac acacacatat atatttctgc atgtatatat
                                                                       180
acataattet ttetatagtt acaggaaata ettettetat aattetgatt ttgacteeca
                                                                       240
tectecacea titacteate cacteattae ctaaatettg gettietite ctatatigta
                                                                       300
aataatccat ccaaacttct agccagtact gtcaggaggg ttcttgctcg agtgagctgt
                                                                       360
taatactatt ttccactgac aacttctgca catcgaggac acagtgtatc tgaagactcc
                                                                       420
getgtatact tecaacaacg ggggcatttt tetttegtag teggeatgae aattacttta
                                                                       480
taggaagact cttcacgaat atcaccacct tctaagttga tgaggaattt ccctttaagc
                                                                       540
togattacat otgoagtest ototogtggt tootgaccag taaagttgac toagaagcca
                                                                       600
tcattaattc attcaa
                                                                       616
     <210> 267
     <211> 341
     <212> DNA
     <213> Homo sapien
      <400> 267
ccattatgta tgtattttct tgaaaaatac ttatttcagc tacttatttt taatagttac
                                                                       60
ttattcttgt tgtattgtca tttgagtttt gtatatattt ttgatattaa ccccttgtca
                                                                       120
catgtataat ttgcaaatat tttctccctt tttttagttg tcacattctg ttcattgtat
                                                                       180
cagattetgt geageagett tttaatttga agtgatetga etgaettgtt etteettttg
                                                                       240
tgtcctggga tatttaggtt aaatcaaaaa acttgctgcc cagaccaatg ttatggggct
                                                                       300
ttcactctat tttttggtag tagtagttta agagttttag g
                                                                       341
     <210> 268
      <211> 367
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<213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (367)
     <223> n = A, T, C or G
      <400> 268
                                                                        60
ttgtagattg gaatagcaaa agtgaatget ntgaccaaaa tttttgccct cctaaataaa
gacgtntcct tctagagagc aaatctatca taaaatgtca aaactagaag agaataaaat
                                                                       120
                                                                       180
gaaaggaaaa aacctagaaa aatatcctaa aatatcaaat gcagtcattt ctaaatataa
                                                                       240
gccataatta tagctttacc tattgttctt attgttccta tgctgcttct acaatgttac
                                                                       300
atcaactata cttagcttta ctctcccaaa atcttggtga tgaagccttc tgagtgtgct
ttccaatgtg ccagaaccag aagggcattc caaggcttcc ccacatttcc tccatttacg
                                                                       360
                                                                       367
qagacaq
     <210> 269
      <211> 270
      <212> DNA
     <213> Homo sapien.
     <220>
      <221> misc feature
      <222> (1)...(270)
     <223> n = A, T, C or G
     <400> 269
caaatetete eeteactaga egtaageent tineteacte teteaatett atgeateata
                                                                         60
gnaangengn tgaggtggat taaaccaaac ccagctacgc aaaatcttag catactcctc
                                                                       120
aattacccac ataggatgaa taatagcagt tctaccgtac aaccctaaca taaccattct
                                                                       180
taatttaact atttatatta teetaactac taeegeatee etaetaetea aettaaacte
                                                                       240
cagcaccacg accetactac tatntcgcac
                                                                       270
      <210> 270
      <211> 368
      <212> DNA
      <213> Homo sapien
     <220>
     <221> misc feature
      <222> (1)...(368)
     \langle 223 \rangle n = A,T,C or G
      <400> 270
ctgaatcatg aataacacta tataatagag tntaaggaac acaagcatta gatgtgatcc
                                                                        60
ttgccccata cccttagatt atgtcagact aaagctgaca attctgccag gctctgaacc
                                                                       120
cctagtgccc ccaacccaaa tcttggaagc aaagaatatg ccctgtcata caactttgta
                                                                       180
caagttgtag taaaacaaag cttaagtttt ctcatctttc tacagcaaat ggtcagttat
                                                                       240
ttaataaaca ctaaaatgct cctaagaatc cattttgagt ttgtttacca aacacattgt
                                                                       300
qcaaqaactq actacacaaa aaqttccttt qaaatttqqt ccacaaattc acttaagqtt
                                                                       360
ggaaattt
                                                                       368
     <210> 271
     <211> 313
     <212> DNA
     <213> Homo sapien
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<220>

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<221> misc feature
     <222> (1)...(313)
     <223> n = A, T, C or G
     <400> 271
aaatttatat aaaactctgt acatgttcac tttattattg cataaacagc ataatcttca
                                                                        60
agacaanngt ttgcaaacac atgtccaatt caggaaaaaa aatttcacgt ttctcgtctg
                                                                       120
                                                                       180
gcttttttct tctttttat ttgtttggga gattcccagc tagtttcaga cttggtctgt
gaaggaggca cactattttg cttggtattt gacttggatt tatctgtctc ttgtagtatt
                                                                       240
ggcggcactt gggaagagct cttgtcagaa tcactttttg ataagattac agatggctcg
                                                                       300
                                                                       313
gtagaagtag cag
     <210> 272
      <211> 462
      <212> DNA
      <213> Homo sapien
      <220>
     <221> misc_feature
      <222> (1)...(462)
      <223> n = A, T, C or G
      <400> 272
aaaaaacatt tattttaata agactattgc naacacatta aaaaaactaa atagtaatat
                                                                        60
tacaaaatct atatacttgc acatttagta tttgtcaatg tgccagaggt tttcttcatg
                                                                       120
                                                                       180
aaatttgact tctttgaagt gaaggetttt ttctatcatc tcttatagct ctgactgaat
aagtettaat getttettea tgttttetat caataggggt aaateeegag geteatatgt
                                                                       240
                                                                       300
gtacaatctg ttagagtatc ttccagctat gtcagctcta actgttaaag aagggtctac
aaacatgatt ctaggcacat attgcccatc aggtgataaa ttcttatcag tggtttcatg
                                                                       360
cataaggttt agcatgatga acttattctg agccatttct tgtatttctt cattttgggc
                                                                       420
aaatactttc tttagtgctt gagagtattg acaatcctcc ag
                                                                       462
      <210> 273
      <211> 282
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(282)
      <223> n = A, T, C or G
      <400> 273
ctgatcaaag catgggatat tttaatagtn ttatacataa tatttttaca tagaaaactt
                                                                        60
tacatnncat ttcatattat ataattctgc ttattctttc aaaaatttat acatccattg
                                                                       120
ggcaaggaat ggttttcatt aaattaccaa tattaaatgc acttaatcat tgtgtatagg
                                                                       180
ttaaaccaaa gtaactatta actaactttt aggcatttta aggaggtaaa acatacattt
                                                                       240
tacacataag tatttgatgc aaatatgcag ataaaatttt tt
                                                                       282
      <210> 274
      <211> 125
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(125)
      <223> n = A, T, C or G
```

```
<400> 274
cagocotaga cotoaactac otaaccaacn tinottaaaa taaaatocoo actatgoaca
                                                                       60
ttnaatcnct ccaacatact cggattctac cctagcatca cacaccgcac aatcccctat
                                                                      120
                                                                      125
     <210> 275
      <211> 528
      <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(528)
     <223> n = A, T, C or G
      <400> 275
aaagctgtgg aaaagcttta ttatagattt ttntacagaa ttaaaaaagt tcaaacaata
                                                                        60
ataagcongg aaccacaaat aattaaaagg aaacacagca atcccataaa caagcattot
                                                                       120
ggcatctgtt agaaattttc cctcaaatta tgaaatgtag ctctccatgc tttccaatga
                                                                       180
ttgttataat acccacaat atctgtgatt tcagtggaat actttaacaa aagttttctt
                                                                       240
tttaaggcat gatcctgatt catttttct tcaatatctc agtcatttca ggaactacct
                                                                       300
taaataaatc tgcaactatt ccataatctg ccacttggaa aattggagct tctgggtctt
                                                                       360
tattaattgc cacaattgtc ttgctgtctt tcatcccagc taaatgttgg atggctccag
                                                                       420
atattccaac agcaatataa agttctggtg ctactatttt tcccgtctgn ccaacttgca
                                                                       480
tgtcattggg aacaaagcca gcatcaacag cagcacggga agcaccaa
                                                                       528
     <210> 276
     <211> 420
      <212> DNA
     <213> Homo sapien
     <220>
      <221> misc feature
      <222> (1) ... (420)
     <223> n = A, T, C or G
aaatgtettg ttteecagat tteaggaaan tttttttett ttaagetate cacagettae
                                                                        60
agaaacctga taaaatatac ttttgtgaac aaaaattgag acatttacat tttctcccta
                                                                       120
tgtggtcgct ccagacttgg gaaactattc atgaatattt atattgtatg gtaatatagt
                                                                     180
tattgcacaa qttcaataaa aatctqctct ttqtatqaca qaatacattt qaaaacattq
                                                                       240
gttatattac caagactttg actagaatgt cgtatttgag gatataaacc cataggtaat
                                                                       300
aaacccacag gtactacaaa caaagtctga agtcagcctt ggtttggctt cctagtgtca
                                                                       360
attaaacttc taaaagttta atctgagatt ccttataaaa acttccagca aagcaacttt
                                                                       420
     <210> 277
     <211> 668
      <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(668)
     <223> n = A, T, C or G
      <400> 277
ccagggtggc tctgatatag cagccctggt ntattttcga tatttcagga agactggcag
                                                                        60
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```
atngcaccag accetquatt ettetagete etceaatece attttatece atggaaccae
                                                                       120
taaaaacaaq qtctqctctq ctcctqaaqc cctatatqct qqaqatqqac aactcaatqa
                                                                       180
aaatttaaag ggaaaaccct caggectgag gtgtgtgcca ctcagagact tcacctaact
                                                                       240
agagacagge aaactgcaaa ccatggtgag aaattgacga cttcacacta tggacagctt
                                                                       300
ttcccaagat gtcaaaacaa gactcctcat catgataagg ctcttacccc cttttaattt
                                                                       360
qtccttqctt atqcctqcct ctttcqcttq qcagqatqat gctqtcatta qtatttcaca
                                                                       420
agaagtaget teagagggta acttaacaga gtateagate tatettgtea ateceaacgt
                                                                       480
tttacataaa ataagagate etttagtgca eecagtgact gacattagca gcatetttaa
                                                                       540
cacaqccqtq tqttcaaatg tacaqnqqtc cttttcaqaq ttqqacttct aqactcacct
                                                                       600
gttctcactc cctgttttaa ttcaacccag ccatgcaatg ccaaataata gaaattgctc
                                                                       660
                                                                       668
      <210> 278
      <211> 202
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(202)
      \langle 223 \rangle n = A, T, C or G
      <400> 278
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                                                                        60
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gagaagtaaa taaagccaat ggcactccct tcagaggctc aaaatggtta gattttgatg
                                                                       180
cagatttaac cttagcgagt ttcagtcagt ccatttagat gatcctgtag gttcatacaa
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atacactgaa ccgttggttt aacttctctt ccttcctcaa agtttatgat aaagagactc
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atccctgtat tgggagtgac tgacataagt tcagatctgc tcagagtggc tggtaaggaa
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cacttaaggt cagtcagaaa ataatcaaac agacttctca tgtaagcacc gtgactcaca
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aaaaaagnet ateceaegen tttntcaeet gggeeeageg gnneteetee nggggggggn
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cgcaatttta ccttctgtct tttcagctac ccaggtgttt atgtgttttc tggacttctc
                                                                      180
                                                                       240
tacggcgctg ataaagtcaa gctcctccat ctctgcttgg tagaattttt ggcaggaatc
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accaquatet tqcacaqett ttqqtqtttq qateataqta ecattttaat atgaaateee
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tqcaaqttcc ttcqtctttc qqcaacttqc atatatctqt ttcaqtqaga gccaatggtt
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                                                                       300
ctqtgctcac cattaqattq atqqttqaac tagaagctqa ccttgctggc tgtggaggtg
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ggggetgaga tttctttgta ctgaaacttc cgtggtaggt ggctctgacc tgagacctca
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cctccatcca gttgttgaag ggtgcagccc gcttggcata ctccaagtac agctggtcaa
                                                                       180
tggtetecag cagttteteg gteegeteca gagetteeet tegettetga gttagggeee
                                                                       240
                                                                       300
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aatantccag ctcattgagc tcctgtgcga tggcggcaat ctgctccaca cggtcctggt
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gggcagccag gccactctcg aagg
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aatagtgggg ctttcaggtg tttagagatt tttttgttg ttgttaacat tcattgcaaa
                                                                       180
                                                                       240
aqtactaqat qqtgtataac tctaqaqttq aattttaaqq gattccctaa tatgtatact
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atcttttat ctgaagtaat aaataaacaa tgatcttg
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tggcctcctt ggcactggtc tcaaagtagg gaatgttgtt tttgctgtag caccagg
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cagtactgtt ggttaaatga caatttatgt ggattttgca tgtaatacac agtgagacac
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agtaatttta totaaattac agtgcagttt agttaatota ttaatactga otcagtgtot
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gcctttaaat ataaatgata tgttgaaaac ttaaggaagc aaatgctaca tatatgcaat
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ataaaatagt aatgtgatgc tgatgctgtt aaccaaaggg cagaataaat aagcaaaatg
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agtattcagg cagatgttac ataactgcta attaagtttc cctggattga ntttanncaa
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anaattgaaa gtngattttg gtcangtgtc agnaaactac tgcctataaa cccatatcnt
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                                                                  120
180
cctgttattg gtagttctga acgttagata ttttttttcc atggggtcaa aaggtaccta
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agtatatgat tgccgagtgg aaaaataggg gacagaaatc aggtattggc agtttttcca
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tttncatttg tgggngaatt tttaatataa atgcggagac gtaaagcatt aatgcnagtt
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397
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tacgagtace caaaattgct gttgtgggga ggcccattgt ggatcatggt ctcatctate
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gggtaggtcg tcttgtcagg gaagatacag gtggacaggc aggacaccac cttgcgggcg
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cccacctega aggccgagtg caggacgttg tcgttcatgt gcacgttttt cctccagaag
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tccaaattgt atttgatatt ccggaacagg ccccccacca ttgcagcaag atggatgacg
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tgtgtgagtt ggaccttctc aaacagggcg cgggtctgtg ctgtatccgt gagatcggcg
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tctttagagg agacaaacac ccagtcc
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ctgttctctt tttcattttc agctctggta agggcaggga ccaccctgca ggaagtgtca
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                                                                     480
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                                                                     180
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gctgctgtgc cttggaaatg annntcggnt gtcanagcct gggaagtggt gggaagaacc
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88

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89

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383
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     <211> 263
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ggcgtttttc agagctgcag ggacagggtg agcagctgaa gggctaggag ggaagccggc
ccccgctctg cagaagctgc atttcagctg aatctgtgtt tcagcctcag ttggttgcac
                                                                      180
cgttagcccc tctcctcccg gatggtcatg tttttgtcac attagagaat aaacagccac
                                                                      240
acacacattt tttttttcc ttt
                                                                      263
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      <211> 132
      <212> DNA
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                                                                      120
taattqatta ttqataactq tcatcatqaa attatctctc aataataaga taaataaact
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agcatatgaa to
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ttctgattct gtttctcagt agtcctttta gaggcttgct atacttggtc tgcttcaagg
                                                                      180
aggtcgacct tctaatgtat gaagaatggg atgcatttga tctcaagacc aaagacagat
gtcagtgggc tgctctggcc ctggtgtgca cggctgtggc agctgttgat gccagtgtcc
                                                                      240
                                                                      300
tetaactcat getgteettg tgattaaaca cetetatete eettgggaat aageacatae
aggettaage tetaagatag ataggtgttt gteettttae categageta etteecataa
                                                                      360
taaccacttt gcatccaaca ctcttcaccc acctcccata cgcaagggga tgtggatact
                                                                       420
tggcccaaag taactggtgg taggaatctt agaaacaaga ccacttatac tgtctgtctg
                                                                       480
aggnagaaga taacagcagc atctcgacca gcctctgcct taaaggaaat ctttattaat
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canctatttg ntcctcctcc cccaccccag nccccaactt catgettntc ttccgcnctc
                                                                       180
agconocoty cootytooto gogytyayto antyacoaon gnttocooty cangagoogo
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gnggccctgt gaaanagctg g
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categgeete ggeeteagtg ceatetgggg teagaacegt geaggteact ttaccettee
                                                                       180
cggcagtctt ggcatcaacc acaaagccta cttcttcgcc agttttcaca gtggaggcga
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ttccaggacc cgtag
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aaaaaagata aggcaagatg cattaaacat gaaaccttct ggctcttttc ctctgcgttt
                                                                       180
ttacagagcc actgatgact atctgcaaca aaagagttaa gtttctgatt ttccgtatca
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agcatcttat gcctttgctg tggtaagaat tctggccaag caccctgaag gacagatgct
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ggtgatggne tttggcactt atgctggcaa actgagcttc tttcccttga gtacttttgn
                                                                       360
aatgtacaag tagaagaagt cacaagtata ggatggtetg gactacgccg gccaccacag
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caatgaggtc aaagaagccc tcaaagnaga agcgnccaga tccagttgac aagatacaaa
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gcacgataga ggccca
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ggccaagecc catgtagece cagteatect geccagece gecteetgg
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ggaccgagaa actgctggag accattgacc agctgtactt ggagtatgcc aagcgggctg
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caccetteaa caactggatg gaggggcca tggaggacet gcaggacace ttcattgtgc
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                                                                       120
ttgnacttgg ncacttttgt gettgaggag geceatttte tgeetggeag ggggeaggta
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tgtgccctcc cgctgactcc tgctgtgtcc tgaggtgcat ttcctgttgn ncacacaang
                                                                      240
                                                                       300
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                                                                       180
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gtctaaagca gttcacagaa aaaatgcagt cagatatgga gaaaatccaa gaattaagag
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actcagtgtg cagaaaaggt ggagtaacct cagcccccca gaatggattc tgggcagtgt
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ctttgtggta tgggaaagaa tattgggctc ttacctccca atgactgccc tacccctgcg
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ggggatctac catctaaatc ttttcatagc ttttcttct cccaaagtgg atccttcctt
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104

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WO 01/49716

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cacgatgttt attttttct ccatgttgta tatcattacc atttcacata cgcgtttcta
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gtgttattta agagatcaaa tgtataacca cctagctctt ttcacctgac ttagtaataa
                                                                       240
ctcatactaa ctggtttgga tgcctgggtt gtgacttcta ctgaccgcta gataaacgtg
                                                                       300
tgcctgtccc ccaggtggtg ggaataattt acaatctgtc caaccagaaa agaatgtgtg
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gttcgtggtt atcccattgt ggaaattcat cttgaatccc attgtcctat agtcctagca
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attt
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gccattatat ttgattttgc attactgttt cacaatqaag ctttctttaa ggctttgatt
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ctcctggcgg caggcagcca tgtgatcatt ctgggtgacc tgaatacagc ccaccgcccc attgaccact gggatgcagt caacctggaa tgctttgaag aggacccagg gcgcaagtgg atggacagct tgctcagtaa cttggggtgc cagtctgcct ctcatgtagg gcccttcatc gatagctacc gctgcttcca accaaagcag gagggggcct tcacctgctg gtcagcagtc actggcgccc gccatctcaa ctatggctcc cggcttgact atgtgctggg ggacaggacc ctggtcatag acacctttca gg	120 180 240 300 360 382
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107

420 tacataacac caattaatga gatcattact gctttatgct ctaattgctt cctgtattca aaatcttctc tccaaccaca taatgactcc ctaaacttct cttgtatttt ccaatgcctt 480 gtacaagcac agaactggtc aatcaataaa tactcactgg ttatttgagg aaaaaatgtt 540 gccaagcacc atctttatca gaaaataaat caattcttct aaacttggag aaatcaccct 600 attoctagta tgtgatotta attagaacaa ttcagattga gaangngaca gcatgctggc 660 agtecteaga gecetegett geteteggna eetecetgee tgggeteeca etttggtgge 720 atttgaggag cccttcagcc t 741 <210> 372 <211> 218 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1)...(218) <223> n = A, T, C or G<400> 372 ccgccagtgt gctggaattc gcccttggcc gcccgggcag gtaccacaac agcaggnctg 60 agtgagaaat ctaccacctt ctacagtage cccagatcac cggacacaac actctcacct 120 gccagcacga caagctcagg cgtcagtgaa gaatccacca cctcccacag ccgaccaggc 180 218 tcaacgcaca caacagcatt ccctggcagt accttggn <210> 373 <211> 168 <212> DNA <213> Homo sapien <400> 373 actgctaggg aatgctgttg tgtgcattga gcctggtcgg ctgtgggagg tggtggattc 60 ttcactgacg cctgagcttg tcgtgctggc aggtgagagt gttgtgtccg gtgatctggg 120 gctactgtag aaggtggtag atttctcact caggcctgct gttgtggt 168 <210> 374 <211> 154 <212> DNA <213> Homo sapien <220> <221> misc feature <222> (1)...(154) <223> n = A, T, C or G<400> 374 tgagaaatct accaccttct acagngagcc ccanatcacc ggacacaaca ctctcacctg 60 ccagcacgac aagctcaggc gtcagtgaag aatccaccac ctcccacagc cgaccaggct 120 caacgcacac aacagcattc cctggcagta cctc 154 <210> 375 <211> 275 <212> DNA <213> Homo sapien <400> 375 actgccaggg gacagtgctg tgtcagttga acctgggctg ctgtgggaag ttgttgattc 60 ctgactgggg cctgaggtgg tggtgctggc aggtaacagt gttgtatccg ttgagcctgg 120

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gctgctgtgg gaagttgtag aatgccgact gaggcctggc gtggtggtgc tgtcagggaa
                                                                    180
tgctgttgtg tgcgttgagc ctggtcggct gtgggaggtg gtggattctt cactgacgcc
                                                                    240
                                                                    275
tgagettgtc gtgctggcag gtgagagtgt tgtgg
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     <221> misc feature
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     <223> n = A, T, C or G
     <400> 376
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ctgactggag cctgaggtgg tggtgctggc aggtaacagt gttgtatccg ttgagcctgg
                                                                    120
gctgctgtgg gaagttgtag aatgccgact gaggcctgcc gtggtggtgc tgntagggaa
                                                                    180
                                                                    191
tgctgctagc g
     <210> 377
     <211> 476
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     <400> 377
cegecagtgt getggaatte geeettggee geeegggeag gtacatttee ttgtagaete
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tgttaatttc ctgcagctcc tggttggttc tggagcagat gatctcaatg agagagtcct
                                                                    120
cgtcggttcc cagccccttc atggaagctt ttagctcaga agcgtcatac tgagcaggtg
                                                                    180
tetteaatag geccaaaate acegteteea ggtggccaga taaggetgae tteagtgetg
                                                                    240
atgcaagttc ctttttggtc cttctctggt aggcgaaggc aatatcctgt ctctgtgcat
                                                                    300
tgctgcggtt ggtcaaaatg ttgacaatgg tgacctcatc cacacctttg gtcttgatgg
                                                                    360
ctgtttcaat gttcaaagca tcccgctcag catcaaagtt agtataggct ttgacagacc
                                                                    420
catatgcact tgggggtgta gagtgatcac cctccaagcc gagcttgcac aggatt
                                                                    476
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     <211> 455
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(455)
     <223> n = A, T, C or G
     <400> 378
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                                                                     60
aatcatattg tcagttgtcc aaagcagctt gaatttaaag tttgtgctat aaaattgtgc
                                                                    120
                                                                    1.80
aaatatgtta aggattgaga cccaccaatg cactactgta atatttcgct tcctaaattt
cttccaccta cagataatag acaacaagtc tgagaaacta aggctaacca aacttagata
                                                                    240
300
agaaacaaat ttcaaaataa atcacatctt ctcttaaaac ttggcaaacc cttccctaac
                                                                    360
tgtccaagtn tgagcataca ctgccactgg ctttagatac tccaattaaa tgcactactc
                                                                    420
tttcactggt ctgaatgaag tatggtgaaa caagc
                                                                    455
     <210> 379
      <211> 297
      <212> DNA
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<213> Homo sapien
      <220> -
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      <222> (1)...(297)
      <223> n = A, T, C \text{ or } G
      <400> 379
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caggtacaaa gaatccttag acqccatact gagttttaag ttccttaatt cctaatttaa
                                                                       120
qqcttctaqt qaaqcctcct cacaqtaqqc ttcactaqqc ccacaqtqcc cctaqacctc
                                                                       180
tgacaatccc accetagaca gactttattg caaaatgcgc ctgaagaggc agatgattcc
                                                                       240
caagagaact caccaaatca agacaaatgt cctagatctc tagtgtggna gaactat
                                                                       297
      <210> 380
      <211> 144
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
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      <223> n = A, T, C or G
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ctatttttt gngtttttt gtttttaaat caataagtaa tctaggacta gcattatgtt
                                                                       120
tgctagacct ggcatttgct cggc
                                                                       144
      <210> 381
      <211> 424
      <212> DNA
      <213> Homo sapien
      <400> 381
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                                                                        60
aactaactga cagcttcatg aaactgtcca ccaagatcaa gcagagaaaa taattaattt
                                                                       120
catgggacta aatgaactaa tgaggataat attttcataa tttttattt gaaattttgc
                                                                       180
tgattettta aatgtettgt tteecagatt teaggaaact tttttettt taagetatee
                                                                       240
acagcttaca gcaatttgat aaaatatact tttgtgaaca aaaattgaga catttacatt
                                                                       300
ttctccctat gtggtcgctc cagacttggg aaactattca tgaatattta tattgtatgg
                                                                       360
taatatagtt attgcacaag ttcaataaaa atctgctctt tgtataacag aatacatttg
                                                                       420
aaaa
                                                                       424
      <210> 382
      <211> 408
      <212> DNA
      <213> Homo sapien
      <400> 382
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aactaactga cagcttcatg aaactgtcca ccaagatcaa gcagagaaaa taattaattt
                                                                       120
catgggacta aatgaactaa tgaggataat attttcataa ttttttattt gaaattttgc
                                                                       180
tgattcttta aatgtcttgt ttcccagatt tcaggaaact ttttttcttt taagctatcc
                                                                       240
acagcttaca gcaatttgat aaaatatact tttgtgaaca aaaattgaga catttacatt
                                                                       300
ttctccctat gtggtcgctc cagacttggg aaactattca tgaatattta tattgtatgg
                                                                       360
taatatagtt attgcacaag ttcaataaaa atctgctctt tgtatgac
                                                                       408
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<210> 383
      <211> 455
      <212> DNA
      <213> Homo sapien
      <220>
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     <222> (1) ... (455)
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                                                                        60
aactaactqn cnncttcatq aaactqtcca ccaaqatcaa qcaqaqaaaa taattaattt
                                                                       120
catgggacta aatgaactaa tgaggataat attttcataa ttttttattt gaaattttgc
                                                                       180
tganncttta aatgtcttgt ttcccagatt tcaggaaact tttttcttt taagctatcc
                                                                       240
acagcttata gcaatttgat aaaatatact tttgtgaaca aaaattgaga catttacatt
                                                                       300
ttctccctat gtggtcgctc cagacttggn aaactattca tgaatattta tattgtatgg
                                                                       360
taatatagtt attgcacaag ttcaataaaa atctgctctt tgtataacag aatacatttg
                                                                       420
                                                                       455
aaaacattgg ttatattacc aagactttga ctaga
      <210> 384
      <211> 376
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(376)
      <223> n = A, T, C or G
      <400> 384
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                                                                       120
aactaactga cagcttcatg aaactgtcca ccaagatcaa gcagagaaaa taattaattt
catgggacta aatgaactaa tgaggataat attttcataa ttttttattt gaaattttgc
                                                                       180
tgattcttta aatgtcttgt ttcccagatt tcaggaaact tttttttctt ttaagctatc
                                                                       240
                                                                       300
cacagcttac agcaatttga taaaatatac ttttgngaac aaaaattgag acatttacat
                                                                       360
tttctcccta tgtgggcgct ccagacttgg gaaactattc atgaatattt atattgnatg
                                                                       376
ggaatatagc attgcc
      <210> 385
      <211> 422
      <212> DNA
      <213> Homo sapien
      <400> 385
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tggtaatata accaatgttt tcaaatgtat tctgtcatac aaagagcaga tttttattga
                                                                       120
acttgtgcaa taactatatt accatacaat ataaatattc atgaatagtt tcccaagtct
                                                                       180
ggagcgacca catagggaga aaatqtaaat qtctcaattt ttqttcacaa aagtatattt
                                                                       240
tatcaaattg ctgtaagctg tggatagctt aaaagaaaaa aagtttcctg aaatctggga
                                                                       300
aacaagacat ttaaagaatc agcaaaattt caaataaaaa attatgaaaa tattatcctc
                                                                       360
attagttcat ttagtcccat gaaattaatt attttctctg cttgatcttg gtggacagtt
                                                                       420
                                                                       422
tc
     <210> 386
      <211> 313
      <212> DNA
     <213> Homo sapien
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111

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atcaatgatt	agaactaaaa	tgtcaaatgc aaaatttggc tagctagcat	ataaaaaaat	cacaattcag	cataaataaa	360 420 473
		en				
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		en				
	acaattctta	gagatgctag tatgccaaat		agctaaaaat	agctttattt	60 98
<2112 <212	> 393 > 397 > DNA > Homo sapid	en .				
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tgccgatata gaactcactt ttgacatgtg aactcttgat aacaagagca cgactaattt	ctctagatga tcctcctgag ccagggcaat tatccatatt ctacattcat caaaatgctt	agttttacat gctttggatt gatgaatgag gagtcaaatg ttagctaaac tttattatta cgatctcaga	tgacattgca aatctacccc gtaggcattt ggattccaaa ttattttta	tttgaccttt cagatccaag cctatcacct gagtagaatt	tatgtagtaa catcctgagc gtttccattc gcattgaccg	60 120 180 240 300 360 397
<212	> 394 > 373 > DNA > Homo sapid	en				
<222	> misc_feat > (1)(37) > n = A,T,C	3) ·				
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ctaaacggat tccaaagagt agaattgcat tgaccacgac tantttcaaa atgcttttta
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ttattattat tttttagaca gtctcacttt gtcgcccagg ccggagtgca gtggtgcgat
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ctcagatcag tgt
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     <221> misc feature
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     <223> n = A, T, C or G
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actaatcacc acccaacaat gactaatcaa actaacctca aaacaaatga taaccataca
                                                                      120
caacactaaa ggacgaacct gatctcttat actagtatcc ttaatcattt ttattgccac
                                                                      180
aactaacctc ctcggactcc tgcctcactc atttacacca accacccaat tatctataaa
                                                                      240
cctagccatg gccatcccct tatgagcggg cgcagtgatt ataggctttc gctctaagat
                                                                      300
taaaaatgcc ctagcccact tcttacngca aggcacacct acacccctta tccccatact
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agttattate gaaaccatea geetaeteat teaaccaata geeetggeeg t
                                                                      411
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     <211> 411
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                                                                      120
caacactaaa ggacgaacct gatctcttat actagtatcc ttaatcattt ttattgccac
                                                                      180
aactaacctc ctcggactcc tgcctcactc atttacacca accacccaac tatctataaa
                                                                      240
cctagccatg gccatccct tatgageggg cgcagtgatt ataggctttc gctctaagat
                                                                      300
taaaaatgcc ctagcccact tcttaccaca aggcacacct acacccctta tccccatact
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agttattatc gaaaccatca gcctactcat tcaaccaata gccctggccg t
                                                                      411
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      <211> 351
      <212> DNA
      <213> Homo sapien
     <220>
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gaggtcaaaa ncaaaaaaaa aaaaaacaaa acnaaaaaaa gaaaaaacca acaattcttc
                                                                      120
aattcagtgt gcaaacatta tataaaaata gaaatactaa ctctacaggc agtatttcct
                                                                      180
gataaattat ttaaatagca tatctacnca atctgagata tctattccaa tggcaatgag
                                                                      240
aaaataattt ataaaaataa agcaatggta taccanatga tagaaaaaaa cataactttc
                                                                      300
agaaattgta tttaacattt caatgctatt tccttattgn gaatncttct c
                                                                      351
     <210> 398
      <211> 363
     <212> DNA
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<213> Homo sapien

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<400> 398
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                                                                   120
tgcaaacatt atataaaaat agaaatacta actctacagg cagtatttcc tgataaatta
                                                                   180
tttaaatagc atatctacac aatctgagat atctattcca atggcaatga gaaaataatt
                                                                   240
tataaaaata aagcaatggt ataccagatg atagaaaaaa acataacttt cagaaattgt
                                                                   300
atttaacatt tcaatgctat ttccttattg ggaatacttc tctgcagagt ttttatgcta
                                                                   360
tqt
                                                                   363
     <210> 399
     <211> 360
     <212> DNA
     <213> Homo sapien
     <400> 399
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                                                                    120
ataaccattg ccccaccatg aacatggggc ttgggaagac agtcctacaa tcttcatcat
                                                                   180
atatttaggt ttttaggcca gccagctctt tttttccaaa gctttctttt gaatacccgc
                                                                   240
ccgggcggcc cctaagggcg aattetgcag atatccatca cactggcggc cgctcgagca
                                                                   300
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     <211> 87
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
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     <400> 400
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ctatattgag tggaattaca atncnct
                                                                    87
     <210> 401
     <211> 328
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(328)
     <223> n = A, T, C or G
     <400> 401
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getgacette ettecaetat tgteetatga eeetgeeaaa teeeeetetg egagaaacae
                                                                    120
180
ccacaaaaaa aaaaaaaag aaagtntata aaataaaata ttgaagtcct ttcccattaa
                                                                   240
aaaaaaaaaa aagaaaaagc acggactctt tcatccagtt ctgatgtgat tatctctgga
                                                                   300
aggeattttc tecteetett ceeteece
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<210> 402 <211> 268

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<212> DNA
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     <221> misc_feature
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catcacaccc cgaagattga gatccactgt atttacacaa agcaaagcca tgtcagcaag
                                                                      120
ggactgtcaa cctgattctg agaacataaa cattcaaaat ttattttcca gtgttccttt
                                                                      180
ttggaaacca acaacacatc tttaatacct acacacacac acatctntac ctttaaaaaa
                                                                      240
aaaaaaaag tgnaacttca cagatagt
                                                                      268
      <210> 403
      <211> 538
      <212> DNA
      <213> Homo sapien
      <400> 403
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                                                                       60
caaggaaaca gaaccacaga aataaataca ttqqttaaca tcagattagt tcaggttact
                                                                      120
tttttgtaaa agttaaagta gaggggactt ctgtattatg ctaactcaag tagactggaa
                                                                      180
tctcctgtgt tcttttttt tttaaattgg ttttaatttt ttttaattgg atctatcttc
                                                                      240
ttccttaaca tttcagttgg agtatgtagc atttagcacc actggctcaa tgcgctcacc
                                                                      300
taggtgagag tgtgaccaaa tcttaaagca ttagtgctat tatcagttac caccatttgg
                                                                      360
ggcttttatc cttcatgggt tatgatgttc tcctgatgac acatttctct gagttttgta
                                                                      420
attocagoca aagagagace attoactatt tgatggctgg ctgcatgcag acatttaaag
                                                                      480
cttttagaga atacactaca ccagggagta tgactactag tatgactatt aggagggt
                                                                      538
      <210> 404
      <211> 310
      <212> DNA
      <213> Homo sapien
      <400> 404
                                                                       60
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<211> 151

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                                                                      120
aaagcttttt agtgatcatt tattactttg tgtttactag atattaattc taagatgaat
                                                                      180
tcctttagaa ttttagaaaa aattattcta gacaacaatc aaagtaaagg atacatccag
                                                                      240
cattgaaacc ataagccggc aagtctccag gttaaaaggt ttgtatcctc cagcaatgcc
                                                                      300
agactgtgtc agacatetet gcaattcate agcatetate tgcccatect gtccagetae
                                                                      360
agcagcaaag taaccataca geggateetg agtttgteeg ggaaaegeag geeeteeggg
                                                                      420
agcccctcca tactgcatct tgagttgaag tcttatangt agaagctggt gatccttaga
                                                                      480
                                                                      481
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     <211> 296
     <212> DNA
     <213> Homo sapien
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                                                                       60
                                                                      120
aaacactcaa aacattttcc attggaaaca tgtaaagaca atatgaggtt ttgttaccat
cttactgcaa ttttcttatg tgttactagt ctacataccc catgttttct gtaatcatgc
                                                                      180
                                                                      240
agatgtgaat ggaagtttga atgattaaat aaatgaaaag tccgtttact gcagggaatc
atttcacaag gcagccaaac cgggtttaga gaacaaaact attcaagaaa ttctcc
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     <212> DNA
     <213> Homo sapien
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     <221> misc feature
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     <223> n = A, T, C or G
     <400> 451
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                                                                      120
cctttcctct cttttaaata attcttcatt gagttctaat atgtaaaaaa aaagtttact
                                                                      180
qtaaaqtttq caaataanqa aattttttt aaaaqtcctc aqtaatctta ccaqtaacaa
                                                                      240
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                                                                      294
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     <211> 129
     <212> DNA
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atagaagag
                                                                      129
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      <223> n = A,T,C or G
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gaccttttta tgagaataaa atgtctattt ctgaaatgtc cctatttctg gaaatgttcc
                                                                      120
                                                                      151
ttatactaaa gtccaacttg tgtggattan t
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                                                                      119
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      <211> 515
      <212> DNA
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      <400> 455
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                                                                      120
gctttatgtg ttactgacac aatatcttcc tcaagctgat gggctttgga tgtagcatca
                                                                      180
ctgaacctct tcttaaactc ttcattttcc atttttaagc tttgtgttac ttcagtaaga
                                                                      240
cccttttgtt ctgcttgcag ttggtcacat ctttctttct catggttaag ttctctttcc
                                                                      300
                                                                     360
attotocoaa ottgttotog aagttgtgot gtttottttt coagaacggo aattaacttt
aacagttett ettittettt catggtttte teaattttea aeteaagaag geetgetttt
                                                                      420
gtggtcacca ctaacatgtc agaatttcct tcatcttcca tagtaagcag ctcttcaact
                                                                      480
ggagaagaag ctcgaaactg gaaaggtgta cctgc
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      <220>
      <221> misc_feature
      <222> (1)...(350)
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gagtagetea etgeteactg etgaggagaa aggeacaaga tataatgtea taagageagg
                                                                      120
acagtggctc agcctacaga gttccctata ggggaaagaa ggcaggaaat aggcgcaggg
                                                                      180
totggtcctg tccctgcacc accctgagca gctagtcttg ggaagggatt acaggccctg
                                                                      240
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129

ggccataggc tgctcqccat tctqctttcc tatcctgttt ctctccctgt qctqctccct 300 tttagccagn gctgagaaat gttcancacc tgaggcaaaa ctgccatagt 350 <210> 457 <211> 293 <212> DNA <213> Homo sapien <400> 457 gcagggccaa cagtcacagc agccctgacc agagcattcc tggagctcaa gctcctctac 60 aaagaggtgg acagagaaga cagcagagac catgggaccc ccctcagccc ctccctgcag 120 180 attgcatgtc ccctggaagg aggtcctgct cacagcctca cttctaacct tctggaaccc acceaceact gecaagetea etattgaate caegecatte aatgtegeag aggggaagga 240 ggttcttcta ctcgcccaca acctgcccca gaatcgtatt ggttacagct ggt 293 <210> 458 <211> 500 <212> DNA <213> Homo sapien <400> 458 actagactec agattaccet ttettaataa atateteagg gtaaggaaag aaagaaactg 60 tatagatata tttaaaatag agaatacttt ccaagcaata catgatgcct ttcctaaaag 120 actctaaaag aaaaagattc tgtaactctc ttttagcacc aaattattgt ttatcttgct 180 ggatatttta tatgaacagt gttaatttag atgcactaaa gcaaaggtag gcaaactaca 240 accatgagtc aaacatggcc acacccattc atttgctatt gtctaagctg gttttgcact 300 acaactgcag agttgaatag atgcagcaga tcctttacag aaaaagtttt ctgacctcaa 360 ttctaaagta attgtagtag ggagctggag gactttcttt ccctttatgg taattttttg 420 agctacaaaa agagccttgc agaaatgggt gaagggatta atcttttaaa aataaatgct 480 atatattagg aaaataaaaa 500 <210> 459 <211> 394 <212> DNA <213> Homo sapien <400> 459 ggtgaaaaga cttgattttt tgaaaggatt gtttatcaaa cacaattcta atctcttctc 60 ttatgtattt ttgtgcacta ggcgcagttg tgtagcagtt gagtaatgct ggttagctgt 120 taaggtggcg tgttgcagtg cagagtgctt ggctgtttcc tgttttctcc cgattgctcc 180 tgtgtaaaga tgccttgtcg tgcagaaaca aatggctgtc cagtttatta aaatgcctga 240 caactqcact tecaqteace egggeettqc atataaataa eggageatae agtqageaca 300 tctagctgat gataaataca ccttttttc cctcttcccc ctaaaaatgg taaatctgat 360 catatctaca tgtatgaact taacatggaa aatg 394 <210> 460 <211> 279 <212> DNA <213> Homo sapien <220> <221> misc_feature <222> (1)...(279) <223> n = A, T, C or G<400> 460 actneegatt gaageeeeca ttegtataat aattacatea eaagaegtet tgeacteatg 60 agctgtcccc acattaggct taaaaacaga tgcaattccc ggacgtctaa accaaaccac 120

tttcaccgct acacgaccgg gggtatacta cggtcaatgc tctgaaatct gtggagcaaa ccacagtttc atgcccatcg tcctagaatt aattccccta aaaatctttg aaatagggcc cgtatttacc ctatagcacc ccctctagag caaaaaaaa <210> 461	180 240 279
<213> Homo sapien	
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accacagcaa ggaccagggg caccaggagg tccaggaggg cctggttgcc ctgggtggcc 660
tggggagccc tcagatcctc tttcacctct gttac
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<211> 73
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cacggeggeg getgeeaggt tgegagggeg geggggetgg ceegtgggee etggggaget 420
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cgcccgcgcc aggtgcgcca cggacga
<210> 467
<211> 183
<212> DNA
<213> Homo sapiens
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ccg
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<211> 129
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<213> Homo sapiens
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132

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<223> n = A,T,C or G
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acnccaang
<210> 469
<211> 243
<212> DNA
<213> Homo sapiens
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<221> misc feature
<222> (1) ... (243)
<223> n = A, T, C or G
<400> 469
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ggggcagtgg ccatggaggc cgtgctgaac gagctggtgt ctgtggagga cctgctgaag 120
tttqaaaaqa aatttcaqtc tqaqaaqqca qcaqqctcqq tqtccaaqaq cacqcaqttt 180
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ctg
<210> 470
<211> 452
<212> DNA
<213> Homo sapiens
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toccagogae gaogecaceg cgcttatgae cgaceccaag eteatcacet ggteteeggt 180
gtgtcgcaac gatgttgcct ggaactttga gaagttcctg gtgggccctg acggtgtgcc 240
cctacgcagg tacagccgcc gcttccagac cattgacatc gagcctgaca tcgaagccct 300
getgteteaa gggeteaget gtgeetaggg egeeeteet acceeggetg ettggeagtt 360
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                                                                   452
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<211> 168
<212> DNA
<213> Homo sapiens
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<221> misc feature
<222> (1)...(168)
<223> n = A, T, C or G
<400> 471
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taccatgtcc atcagggtga cccagaagtc ctacaaggtg tccacctctg gccccegggc 120
cttcagcagc cgctcctaca cgagtgggcc cggttcccgc atcagctc
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<210> 472

133

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<211> 479
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1) ... (479)
<223> n = A,T,C or G
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catgcagtgc ttcagcttca ttaagaccat gatgatcctc ttcaatttgc tcatctttct 180
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catcgcagcc ggcgttgtgg tntttgctct tggtttcctg ggctgctatg gtgctaanac 360
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<210> 473
<211> 69
<212> DNA
<213> Homo sapiens
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<211> 155
<212> DNA
<213> Homo sapiens
<400> 474
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gtccagagag ccgcggcgcc tcgttccgag gagccatcgc cgaagcccga ggccgggtcc 120
cgggttgggg actgcagggg aaggcagcgg tggcg .
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<211> 282
<212> DNA
<213> Homo sapiens
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tcaaaagcca aaaaatggga gacaatttca catggacttt ggaaaatatt tttttccttt 180
gcattcatct ctcaaactta gtttttatct ttgaccaacc gaacatgacc aaaaaccaaa 240
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<210> 476
<211> 434
<212> DNA
<213> Homo sapiens
<400> 476
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..

134

gtagagcatg tecaegatgt tggagegete etectegtae acegggatge gegtgtggee 180 getetgeatg atgetggeea ggaegeegaa gteeageacg gtgetggegt ceageatgaa 240 gcagtcttcg aggggcgtga gcacgtcctc cacggtccgg cagcgcagca cgcccttgct 300 gagatcgctg taggggtcgc cgccgccgcg cgccagctcc agcacccgct cccgcagccg 360 cccgggccgc gccgccagct ccagcagctg ccccacgggc agcgcgacgg gcagagtgag 420 caggacggcc aggc <210> 477 <211> 314 <212> DNA <213> Homo sapiens <400> 477 ggcgggcgct agctggctcc gggcagctcg gccttggggg cttcggggcc ccgagacgcg 60 gggcgtatga gtggggcgtg cgctccacgc ggaagtcgga gcctcctccc ctggataggg 120 tgtacgagat ccctggactg gagcccatca cctttgcggg gaagatgcac ttcgtgccct 180 ggctggcgcg gccgatcttt ccgccctggg accgcggcta caaggaccca aggttctacc 240 gctcgccccc tcttcacgag catccgctgt acaaagacca ggcctgctat atctttcacc 300 acceptagece cett 314 <210> 478 <211> 317 <212> DNA <213> Homo sapiens <400> 478 aacagagtga tcattccagt taagcggggc gaagagaata cagactatgt gaacgcatcc 60 tttattgatg getaceggea gaaggactee tatategeea geeagggeee tetteteeac 120 acaattgagg acttetggcg aatgatetgg gagtggaaat cetgetetat egtgatgeta 180 acagaactgg aggagagag ccaggagaag tgtgcccagt actggccatc tgatggactg 240 gtgtcctatg gagatattac agtggaactg aagaaggagg aggaatgtga gagctacacc 300 gtccgagacc tcctggt 317 <210> 479 <211> 171 <212> DNA <213> Homo sapiens <400> 479 aggtgctttg ctagatgctg tgacaggtat gccaccaaca ctgctcacag cctttctgag 60 gacaccagtg aaagaagcca cagctcttct tggcgtattt atactcactg agtcttaact 120 tttcaccagg ggtgctcacc tctgccccta ttgggagagg tcataaaatg t <210> 480 <211> 65 <212> DNA <213> Homo sapiens <400> 480 cccccagtgg aaggctccca ccctggtaga tgaacagccc ctggagaact acctggatat 60 ggagt <210> 481 <211> 207 <212> DNA <213> Homo sapiens <400> 481

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ctgacaaccg gcagattgtc tctggat
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<212> DNA
<213> Homo sapiens
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<223> n = A, T, C or G
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tacaagcccc ggatttacac ctcgcccacc tggagtgcct ttgtgacaga cagttcctgg 120
agtgcacgga agtcacaact ggtctatcag tccagacggg ggcctttggt caaatattct 180
tetgattact tecaageece etetgaetac agatactace cetaceagtg ettecaaact 240
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eccaccatec agagetget
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cccgggcccg ctcctcaaca gtcaccgagc tgcggcggga gcagccccct tcagagctgc 180
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<211> 194
<212> DNA
<213> Homo sapiens
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qatagatagc atgtaagggg gtggttgtcc caggaggcag ctgctgacag gtttgctaca 120
cacageceeg gactgtgttg cetgggtget catteagaga ggggetatea tetgggagee 180
tgtgcccctg ggtc
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<210> 485
<211> 67
<212> DNA
<213> Homo sapiens
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tocatatoca ggtagttoto caggggotgt toatotacca gggtgggago otoccactgg 60
gggaagt
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       <211> 257
       <212> DNA
       <213> Homo sapien
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tttcaccgct acacgaccgg gggtatacta cggtcaatgc tctgaaatct gtggagcaaa
                                                                        180
ccacagtttc atgcccatcg tcctagaatt aattccccta aaaatctttg aaatagggcc
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cgtatttacc ctatagt
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       <213> Homo sapien
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agcaattgga cttgtggtaa aaccatccag gagcacagct gggtctcatg atgatatcac
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ccaggactcc tgttttggcc aggcagctca gcaataggag cagccgcatg cttctggaag
                                                                        240
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                                                                        300
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agggcccctg ccttcttc
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       <211> 429
       <212> DNA
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aaactataca gcctaccatc aacagttgtg cattataaaa aggtagtttc tttccttttg
                                                                        180
ttttaagtca ggaacaggta gatttttaaa aatatatata caagctaaca cacacrgcta
                                                                        240
tcagcactaa tgccccccc tcaacttttc ctttttctta tagaaaatgg aaagcttaca
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atacctcstc srtymwrgmr scagrcctwc gagccwgcct grasagggtk wgcmktggar
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<210> 49 <211> 42 <212> DN <213> Ho	2			·	
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<210> 49 <211> 31 <212> DN <213> Ho	8		·		
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318
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actttgggag gccgagccag gtggatcacg aggtcaggag atcgagacca gcctggctaa
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catggtgaaa ccctgtctct actaaaaata caaaaatgag ccgggcatgg tggggggca
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ccgtagtccc agctacttga gaggctgaga caggagaatg gcgtgaaccc ggggggcgga
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gettgtagtg ageegagate gegeeactge aetecageet gggtgacaga gtgagactee
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      <212> DNA
      <213> Homo sapien
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                                                                       120
gtttggttag tgactgatgt aaaacggttt tcttgtgggg aggttacaga ggctgacttc
                                                                       180
agagtggact tgtgtttttt ctttttaaag aggcaaggtt gggctggtgc tcacagctgt
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aatcccagca ctttgaggtt ggctgggant tcaagaccag cctggccaac atgtcagaac
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tactaaaaat aaagaaatca gccatgaaa
                                                                       329
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      <211> 292
      <212> DNA
      <213> Homo sapien
     <220>
     <221> misc feature
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ctctggtttc attgtttcat tgatttcatt gttttgattg atgctgacct taggcagcag
                                                                       120
agttttcaat gctctccagg tgtttctaaa gtgcagacaa gtttangacc gtgcttgagg
                                                                       180
gtgaagggca ggactgtgat ggggaggggc aaatatgggg cccttggggt gcaggcaatg
                                                                       240
gttttccttg acctgaatgg gggtctcaca ggtgttgcat atacatatac gt
                                                                       292
     <210> 497
     <211> 549
     <212> DNA
     <213> Homo sapien
     <400> 497
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tetteettte tgetageetg getaaatetg eteattattt cagaggggaa geetageaaa
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aaactttag 180 tccacagta 240 tgcatctcc 300 agaaggaag 360 tctctccat 420 atgggaagg 480 aaaccattg 540 549
tccagcctg 60 actcttgtc 120 gcaccaggg 180 ttatgcggg 240 ctcttaacc 300 actccccaa 360 c 412
gttgtaacc 60 ctataaaat 120 agtctacaa 180 actttatag 240 caggccact 300 gaatttttg 360 aataaaata 420 447
tttgtgatg 60 tgcacacat 120 ttcacatgg 180 atatactaa 240 ttctgatat 300 aagtcactt 360 tccctttaa 420 aacaacaaa 480 527
t t a t a a a a a a a a a a a a a a a a

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cctgcaagat ggacacgagc cacaagctgc actgtgaacc tgggcactcc gcgccgatgc
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caccggcctg tgggtctctg aagggacccc cccccaatcg gactgccaaa ttctccggtt
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caactgcttc attaaacatt ctgcattggg tataatctaa gaattgttta caaaaagatt
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attitigtatt taccetteat teettittit gateettgta agittagtat aaatatatet
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agacattcag actgtgtcta gcagttacgt cctgcttaaa gggactagaa gtcaaagttc
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ettgtctcac tatttgatct gctttgcagg gaaataactt gttttttctc atgtttcatc
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tgccctgctg cggccagcct gactagaccc caccctgagg tcctgcattt ctcagtcggt
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gtgtaatcac gttccagggc ccaaagccca gctctttgtt cagttgactt actgtttctt
accttaaaaa gtaattgtag atggaaatca gttgtgtttg gcangagaat caataaaaat
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ctttgattca gacagc
                                                                       256
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     <221> misc feature
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                                                                       120
aatgcaaaat aagtcatctt gcatacaggg agtggttaag taaggnttca tcacccattt
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agcactgett ttctgaagac ttcagttttg ytaaggagat ttaggttkta ctgctttgac
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tggtgggcct ctasa
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141

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tgaaaatatt aaaatagcat cgtttattat tttttaatga gtcatgagct catttctaaa
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                                                                      420
gcttcataaa gcattacact gataacatat gtgtggtcag gacaaactgt tccctgaact
taagaggtga aggacaagac cccatattat tatcctgtat taaaaaagga aatatacata
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                                                                      485
tatgt
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     <211> 230
     <212> DNA
     <213> Homo sapien
     <400> 506
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aatgtcacca ctatctggag atttcgacgt gttttcctct ctgaatctgt tatgaacacg
                                                                      180
                                                                      230
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     <211> 179
     <212> DNA
     <213> Homo sapien
     <400> 507
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ggcaaactct cctctttga ggagaagatg atctcggatg ccatccccga gctgaaggcc
                                                                      120
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                                                                      179
     <210> 508
     <211> 321
     <212> DNA
     <213> Homo sapien
     <400> 508
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aatggaatca aaagaaagtt aatttatgaa attaagaggt cagcagaata tactcagtga
                                                                      120
tggaagacac ttgggaaagt ctttttaata gaacaagaac gatcttaatt taagaatatt
                                                                      180
atcctggttt aacaacagtg ccctgtttac aacagattgt gccctatctc atctgcagcc
                                                                      240
gaggaataaa ggattctgat tagaaagagg gttgcctaca gattagtaag caattccttg
                                                                      300
                                                                      321
gatcttatgc acagaacttg t
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<210> 509 <211> 176

<212> DNA

<213> Homo sapien <400> 509 acgtgggata cgggtcatgg gcagagctcc tggcctcagt gatgcctcct gatctatcca taggcctgga agatcagcac tgggatgacg atgagcagaa tggtcatgag gatgcccasa 120 atcagggccc acatgttcag gcacttggcc ggtggatgca targcctggg cccctg 176 <210> 510 <211> 298 <212> DNA <213> Homo sapien <220> <221> misc feature <222> (1)...(298) <223> n = A,T,C or G<400> 510 accaacttta tatcatatgt ttatacaatt taatttaaaa attcattta aggaagacag 60 ataatttgaa agacttttgt ttttcttgac ttaattcatg aagtatcatt ttttgactga 120 gtctccattt acttcattct taatgattat tgtcatccct ttaaatctgt gcctttttct 180 240 tettgagega agetgtttga gtaaacetgt tgaagagtgt ttgtgtettt tgtgettttt tgttgntatt aaaacaccaa ctaaacctta tagtcaagac aaggctctat gtttctgt 298 <210> 511 <211> 345 <212> DNA <213> Homo sapien <400> 511 acagattttt gtatagctga taagattctc tgtagagaaa atacttttaa aaaatgcagg 60 ttgtagettt ttgatggget acteatacag ttagatttta cagettetga tgttgaatgt 120 tectaaatat ttaatggttt ttttaattte ttgtgtatgg tageacagea aacttgtagg 180 aattagtatc aatagtaaat tttgggtttt ttaggatgtt gcatttcgtt tttttaaaaa 240 aaattttgta ataaaattat gtatattatt totattgtot ttgtottaat atgotaagtt 300 aattttcact ttaaaaaagc catttgaaga cctaaaaaaa aaaaa 345 <210> 512 <211> 459 <212> DNA <213> Homo sapien <400> 512 60 acttatttca acaattctta gagatgctag ctagtgttga agctaaaaat agctttattt atgctgaatt gtgatttttt tatgccaaaa tttttttagt tctaatcatt gatgatagct 120 tggaaataaa taattatgcc atggcatttg acagttcatt attcctataa gaattaaatt 180 gagtttagag agaatggtgg tgttgagctg attattaaca gttactgaaa tcaaatattt 240 atttgttaca ttattccatt tgtattttag gtttcctttt acattctttt tatatgcatt 300 ctgacattac atatttttta agactatgga aataatttaa agatttaagc tctggtggat 360 gattatctgc taagtaagtc tgaaaatgta atattttgat aatactgtaa tatacctgtc 420 acacaaatgc ttttctaatg ttttaacctt gagtattgc 459 <210> 513 <211> 422 <212> DNA <213> Homo sapien <400> 513

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<210> 514 <211> 326 <212> DNA <213> Homo sa	pien				
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aagaggatte etetatatat titaaattit aatttattet attteetgat teacaaacte
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                                                                       360
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ncaagcacca ntcaaatate gnantenatt aaaagnaggn ettteecatt tgtngeenge
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teacceanne gtggategtt ggeattgtgg gaaaagggaa accgnaacgg ceeggateat
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cageceageg aggetgggte gggggteact ceaggatgtt ceaaceacag gggeageate
                                                                      120
tectecacte cacatgetgg ccaagggcac agagetgeeg tategeetge caagggggtg
                                                                      180
gctcaatgct gctgccctgg tcctgtatgg gcccggggtg ccgagaacag acagcaagcc
                                                                      240
tcaggcgccg gtcctttgag ctttcttgat ttcctcagag agcgcctcct tcagctctgc
                                                                      300
gtaggcctgg tccaggctgt cgttaatgat gaccacatca aacaggccgg gctccttgct
                                                                      360
gctctccatg tcggcctggg cagcagccag ccgcttcacc aggctctcct cggtttcagt
                                                                      420
gttgc
                                                                      425
      <210> 590
      <211> 425
      <212> DNA
      <213> Homo sapien
      <400> 590
acaagtatac atataatcta gataagggct gtaatgtttc ctaatattaa ttactgtact
                                                                       60
taaaaattta caggacatga acataaataa agctgtttaa aactggcaaa cgtagtaata
                                                                      120
gtctgtcatt cagtacaagg tatatttatg ttatttccaa agccatcacc ctaaaatcct
                                                                      180
aagttgccac tcttaaaacc taaaaataat gtcgaaaact aaagtcataa atacatgtat
                                                                      240
acatacattt gcatatttac acttatgcag aaatcatcaa tatactagag cccagcttta
                                                                      300
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acactgtcct tcagtttcac aggttaaagg gaaaaggtgt caccc					360 420 425
<210> 591 <211> 425 <212> DNA <213> Homo sapie	n				
<pre><400> 591 aagtatgtat gtacaagact ttcagattt actgtggaag tttaacgatg gagtccaagt ggtcaaattt caagattggt cactattaca aatatatgat cccacgcaca cacatttgta aaattatata gttatgcatt ttctc</pre>	catatttaat tctggatttt aaagccagtt gttaaactaa atttgtgtcc	gcacacattt acattagatc tcaagctgct caaactcatg atttgctatt	gaatgttaca tgcatatata tatattttga accttcaaag tcccttcttc	cataaataat agacacttgt gtacaggttt atgtcttcgt tataatcttc	60 120 180 240 300 360 420 425
<210> 592 <211> 299 <212> DNA <213> Homo sapie	n				
<400> 592 agtgaaaatg ggttggtttt tctgttgtga cagacacggg tcctggggcc ggcgaggccc gggtgtgctg tgctgagcgc ctgttgtaga tttatgtaaa	gageteegeg ctteagtett tgtateeetg	tgccagcctg gttctggggg aatatagttt	tggctgccct gacggcccac atttttcta	gctgtggggg tccggggagg catttgaatt	60 120 180 240 299
<210> 593 <211> 425 <212> DNA <213> Homo sapie:	n				
<pre><400> 593 tttttttttt tttttcccag aagcgtctce agctgaagce cgatgagcce ccgccgtgcg gcgccgacga tcgctgccgt ctcccttacg gggctcacaa ctacgccctc aatctgctct gatggcctgg ttgaacgtcc ttgcc</pre>	aatgcagccc tccccgacta tttgcccttg tggccagaaa tttggaatca	tccggctctc tccccaggcg ggagtaggat agattccgtg tcacattcca	cgcgaagaag ggcgtgggc gtggtgaaag aagtgtctgc cttctaaaag	ttecctgece accgggecea gatggggett getgeetget gagetttaaa	60 120 180 240 300 360 420 425
<210> 594 <211> 425 <212> DNA <213> Homo sapie	n				
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163

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caagatttgg tgagggtccc cctctgcctc tcacagaagc ccctggccct ggactgtcct
                                                                    420
ggggg
                                                                    425
   <210> 595
     <211> 162
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(162)
     <223> n = A, T, C or G
     <400> 595
ctttacatta tttttttcc aaaaagacta gtatttatac aangggcaat agaaacaaaa
                                                                    60
acaaaaaccc ttccgactgc cacctggaag gggctggctg gnctgctccc tctcccacct
                                                                    120
ggaacngggg ggggcactgg gcaggaggga atgnggangn gg
                                                                    162
     <210> 596
     <211> 283
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(283)
     <223> n = A, T, C or G
     <400> 596
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                                                                     60
gttaccetet teeteetttg teetetgtge ttgggeteae aacttnatgg netgnacttn
                                                                    120
ataaaanaac natggcaact ttgncctgan tgncnccctn cccaanctga nctggntgga
                                                                    180
anaagaaact tggaaactat ntnanccatg gntttgggan nctncccct tncccatgnc
                                                                    240
tnctaataaa accatgcant gcctttggag agaagagacc ccc
                                                                    283
     <210> 597
     <211> 426
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc_feature
     <222> (1)...(426)
     <223> n = A, T, C or G
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                                                                     60
tcatttttta aatatttttt ttactgccta tgggctgtga tgtatataga agttgtacat
                                                                    120
180
tttctttttc atgatgnggn acctccnaag ngatggnaga tttaaataat tttttatttt
                                                                    240
tattttatat atttnttcat tagggccttt tctcccnaaa acgaaanaaa aantccnaaa
                                                                    300
aacnaaaccc aaaaaaanag agggtantgt conagtttct gtatgtataa agtontnonc
                                                                    360
gatttcagga gagcnctgnn cccaatttgc tccntgaatc aaggngngna aatggttttt
                                                                    420
ttggcg
                                                                    426
     <210> 598
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<211> 412

<212> DNA

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<213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(412)
      <223> n = A, T, C or G
      <400> 598
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                                                                        60
aagagaaaca acataaagag aatatttcaa atccccacaa tttccttctc aacctcacta
                                                                       120
ctcttaacat ttctttatca gacqccactg gcttcctaaa atggaccctg gactatgtat
                                                                       180
ggggaccaca ttcattatgc tqcctttcct cttatgatta aaactttagc cctcattcga
                                                                       240
nggttccaat ggtactttta gnggaggagt ccctagcttt taaaaaaacc acttttcctn
                                                                       300
taaaatccnt tntttatnga aaaaaancnt ttttaaaaat gttaaggagg attttaaatg
                                                                       360
accatattca attaaaaaaa aaatnoottn tggaacatnt tngcagaaac ct
                                                                       412
      <210> 599
      <211> 415
      <212> DNA
      <213> Homo sapien
      <400> 599
ccaagatgac aaagaaaaga aggaacaatg gtcgtgccaa aaagggccgc ggccacgtgc
                                                                        60
agectattcg ctgcactaac tgtgcccgat gcgtgcccaa ggacaaggcc attaagaaat
                                                                       120
tegtcatteg aaacatagtg gaggeegeag cagtcaggga catttetgaa gegagegtet
                                                                       180
togatgocta tgtgcttccc aagctgtatg tgaagctaca ttactgtgtg agttgtgcaa
                                                                       240
ttcacagcaa agtagtcagg aatcgatctc gtgaagcccg caaggaccga acacccccac
                                                                       300
cccgatttag acctgcgggt gctgccccac gtccccacc aaagcccatg taaggagctg
                                                                       360
agttettaaa gaetgaagae aggetattet etggagaaaa ataaaatgga aattg
                                                                       415
      <210> 600
      <211> 208
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(208)
      <223> n = A, T, C or G
      <400> 600
aaaccgcctt ttttttttt tttttttaa tatgcagttt gtaanaacaa aactggatgg
                                                                        60
catcanaatt gtctggaagt tttgtcttgg gcagtatggg ctgggccaaa tgaaatgatt
                                                                       120
tttataattc taaacaggtt accaaatgaa atgtcatggc tttactttgg caattaaagg
                                                                       180
ggggaatttt tttaaaaaaa aaaaaaaa
                                                                       208
      <210> 601
      <211> 165
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(165)
      <223> n = A, T, C or G
      <400> 601
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                                                                        60
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ctagggcaga gaacccagga tgggacacta aaaaaatgtg tttatttcat tatctgcttg
                                                                       120
gatttatttg tgtttttgta acacaaaaaa taaatgtttt gatat
                                                                       165
      <210> 602
      <211> 416
      <212> DNA
      <213> Homo sapien
      <400> 602
aaaacggttt tgccgagttg ggacgtccac tgctgtcaag tcaaccagag atttgaactg
                                                                       60
tgcattggtg tgatccctga ggaaagtcag cactgggatg acgccatcag gatggataca
                                                                       120
gacctctaac tcattgaagc aggacacctg aacttgttgg acatacttgg gcaagatttc
                                                                       180
agccacatac totocaaaag otgagagotg ottgtgggcc acatcattcc gtggtotgac
                                                                       240
agtggggege gtgteggeee eggegetete eegeeteace ggeageaaca gaacggaggg
                                                                       300
togeccagte eccetggtea gegeogagge ecceaagate ecgegocace acageetgge
                                                                       360
taccgccgcc gcgagtactt ctagagcggc cgcgggccca tcgattttcc acccgg
                                                                       416
      <210> 603
      <211> 416
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (416)
      <223> n = A, T, C or G
      <400> 603
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                                                                        60
cttaaaatga agaattettt caaaatttta cgttttttnc attettgget caattetttt
                                                                       120
gettteetea teateagaat teaaaetttg ggeaaaeatg ggttttggge tgantetttg
                                                                       180
gaatatgctg gaaaaacccc aatatgggct gcttctgctt gtttggcatg acgcaaaatg
                                                                       240
gnttcccang atactgcatc gtcttgccaa gaatgttcca ttagaaaaag gcccqqqtcc
                                                                       300
tegecacact ggetggeete tgetgggtge ntetagagta tateggetge aceteagtge
                                                                       360
atctgtccat aatttttttg aaaaaaaaaa ctcaatctta acgcgggcat attcnc
                                                                       416
      <210> 604
      <211> 414
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(414)
      <223> n = A, T, C or G
      <400> 604
aaaatttatg agctttatta aagcggttta tcacaaagat qqaaacqtac aaatqaqaaq
                                                                        60
catgcaacca tcatcttcca cagtcaagtc aaactgctat ttctctctct ctcctgtttc
                                                                       120
atagagetgg aaactgeagg tgttataece aacetattea teeteaacae tqtaqteaeq
                                                                       180
ccccggaaac tactcagggc accaaacatc caaaacataa actattatta tacaaaqaaa
                                                                       240
gtgcaaagtt aaaaaagaaa acatggagac ceetceeec cataceetca netaaaqqet
                                                                       300
aacaatggca cttgggctct tgcttaatct agattgtctt caaaaagtct ctaaaatgng
                                                                       360
atactgngng nggnggggg ngngaanggt ccaaaagctn cttagtgttt gaaa
                                                                       414
      <210> 605
      <211> 417
      <212> DNA
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<213> Homo sapien
      <400> 605
tcctctttca caatcactca acaaacaggt cacacatccc ctaggtccac gaactcatct
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tctcgtttgg ccaaatcgtc ttcatctccc aaagctttcc agccactggt gggtaagacg
                                                                       120
ggcttagagg aatgtcgctg gagcagagcg aaaggaaaca aagacgagag gcgggcagag
                                                                       180
ttcctcagca ggcaggggc ctcagcctgg ggggcctgct ggctgtggtg tctctcgtcg
                                                                       240
atcttctctt gtaaactctg gacttectcc atcatttcca agagtttgct cagagtggcc
                                                                       300
acttggccac cacctaggat ttgggcttct ggaatccaac gtaggtagcg ctgggcccag
                                                                       360
actttgattt cgggcccctc gatatgcggt aacaacaaac catggtagtc agtggac
                                                                       417
      <210> 606
      <211> 413
      <212> DNA
      <213> Homo sapien
      <400> 606
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                                                                        60
ataagttgca tataaaaccc gacctcattg ctcattgtgg taaagcaagg atgatgagaa
                                                                       120
aatgcacctc aggagcaaaa acacgcttta cgggcactcc gggacccaag tcccgagaca
                                                                       180
tttccacgtg accttctgga aagacacacc gcccacctga ctgcacgacg ggactggtcc
                                                                       240
agcetecegg etecteagga aggagatgag ttteetacaa agtgagtgge cacageteea
                                                                       300
ggacagggcg tccacatgtc gttgtgggtc tggctggatt ttgaggtgcc gaggaactgg
                                                                       360
teggtgteet gategtattg tacgtggtge tetegatete ceaactgeea taa
                                                                       413
      <210> 607
    . <211> 414
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
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      <223> n = A, T, C or G
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                                                                        60
gtcacttttt atcatgttaa ctaattgttc tcttttgaag atctatggtt gactaattaa
                                                                       120
acaataattc aagtagagtg tcccagaaaa aaaccacttg ggctccctgt ttggagtctg
                                                                       180
getggetetg ageattgeea atggeeecta eteacetgae tttgtateet eteettttag
                                                                       240
aggetttgca ttetgcacce agetteacta acagtggget gaaaacatee ttgggttgag
                                                                       300
tgtttcattt gggagttatt tggccagggc cttttgaaca gtaagtgtcc ccatgaagtg
                                                                       360
ctagataata tatggngtaa agangtcagc ttttttttt tttttaactc taac
                                                                       414
      <210> 608
      <211> 415
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc_feature
      <222> (1)...(415)
      <223> n = A, T, C or G
      <400> 608
gcagtggtct gatcttaagg gnctatatat ttgcacctcc tcattcaaca cagggctgga
                                                                       60
ggttctacaa caggaaatca ggcctacagc atcctgtgta tcttgcagtt gggattttta
                                                                       120
aacatactat aaagtctgtg ttggtatagt acccttcata aggaaaaaat gaaqtaatgc
                                                                       180
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ctataagtag caggcctttg tacctcagtg tgaagaga tacaatggaa gtggcctcat ggatgaatcc ggggtatc tttggtnacn tatccctttt tntcttaaga aagcangg ttaaaaaatg gnaagcaaac nacaggtgcc tttanaaa	rag cccagganaa cgtgctgctt 300 rtn ctntcttatt annaaatatg 360
<210> 609 <211> 420 <212> DNA <213> Homo sapien	
<pre><400> 609 ggttttaaaa ttatttettg aateteteea tacacagg catactggaa attgeetaac ttaateattg cetaaagg tgettaacea ggaggeeaat geatttgeeg aceteeag gacagaetgt ceaceatetg aaceteatt caceaceg cagateagea geacatttet tgeeaacaat cattaagg atettetgee acagaaatet gggatatatg tttettgg tgettgaggg gaaatgteat ggaaageaag geaceggg</pre>	ag agaaaattat ccccaaaacg 120 aga acatggagat gaacgtgata 180 att cgataaccct tattcaggcc 240 agt ccaagaagac tttcatcatc 300 agt atcaccagaa aatgtgttgg 360
<210> 610 <211> 158 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(158) <223> n = A,T,C or G	
<pre><400> 610 caactttaaa aaaaaggggg cggtnaaana nccaaana aaaggnceet tteegggace ggneenggae ceaeettt ggtaaaceaa geetttaaag cgttgggggt taaattte</pre>	gg gcccaaaggg ggatttaccg 120
<210> 611 <211> 159 <212> DNA <213> Homo sapien	
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<pre><400> 611 tcgacactag tggatccaaa ggaagatggc ggacattc gcagccgacc atctttcaaa acaagaagag ggtcctgc gctcccgcgg tnctacaaga acatcgntct gngnttca</pre>	tg ggagaaactg gcaaggagaa 120
<210> 612 <211> 419 <212> DNA <213> Homo sapien	
<pre><400> 612 gcatttttta ttaagacatt tggggcccga gtttcctc ctctctaaat tcagcttttg gaaacctaag tgtgccca gcctccgggg tccctcttcc ttccttctt ctccccag</pre>	cc ttccccagca ggtagccaga 120

ctgctgtcag cagagggtga agcgt ccgcagcggt ggggccagag gcaag ctcatccaga agctcctggt gcagg ggcccgcagc ctgagcagct gccct	ccagt cccagactct tgaca gacttggtcc	aactccatct actttcagtc	ccagctcagc tgtgcagccg	240 300 360 419
<210> 613 <211> 419 <212> DNA <213> Homo sapien				
<220> <221> misc_feature <222> (1)(419) <223> n = A,T,C or G	·			
<pre><400> 613 ccccatactg aggcatataa agttt tataaaatct gggttaggct aaaac caatcatcct gtctcatctt catta tggcttctta taaagatctt taatg gcttatttgg agaatgctgc taaga ctgcttgagg tacagcagtt tcaa ccaccttaga gcaaaaacct tcaga</pre>	ttatt atgtagacca tttct ggctttatga gagta ttttaaacat atggg attgactgac tccca atgtgtaaag	gagaggcgtt gcagaatgtc tggaaaatcc ataacttact tgcttagaag	gattttaaac etgetaeett atgagtttga ageetettte ttateaetee	60 120 180 240 300 360 419
<210> 614 <211> 123 <212> DNA <213> Homo sapien				
<220> <221> misc_feature <222> (1)(123) <223> n = A,T,C or G				
<400> 614 gnggtatgga ctagaaaact tggaa catgataggg aaantnattc tgagg ntt				60 120 123
<210> 615 <211> 362 <212> DNA <213> Homo sapien				
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<210> 616 <211> 210 <212> DNA <213> Homo sapien				

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<220>
      <221> misc_feature
      <222> (1)...(210)
      <223> n = A, T, C \text{ or } G
      <400> 616
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                                                                       60
cgccagcctc agccaggtgg gcctgtatat agggtccatg tgcaataggg agggacgtct
                                                                       120
totatttttt gctgcccct ccccgcccac tgtctngggg cagggggaga aggtattttc
                                                                      180
nagataaagc acangcacca caaataaaag
                                                                       210
      <210> 617
      <211> 511
      <212> DNA
      <213> Homo sapien
      <400> 617
acgagettte gtggeteact ceettteete tgetgeeget eggteacget tgtgeegaa
                                                                       60
ggaggaaaca gtgacagacc tggagactgc agttctctat ccttcacaca gctctttcac
                                                                       120
catgcctgga tcacttcctt tgaatgcaga agcttgctgg ccaaaagatg tgggaattgt
                                                                      180
tgcccttgag atctattttc cttctcaata tgttgatcaa gcagagttgg aaaaatatga
                                                                      240
tggtgtagat gctggaaagt ataccattgg cttgggccag gccaagatgg gcttctgcac
                                                                       300
agatagagaa gatattaact ctctttgcat gactgtggtt cagaatctta tggagagaaa
                                                                      360
taacctttcc tatgattgca ttgggcggct ggaagttgga acagagacaa tcatcgacaa
                                                                       420
atcaaagtct gtgaagacta atttgatgca gctgtttgaa gagtctggga atacagatat
                                                                       480
agaaggaatc gacacaacta atgcatgcta t
                                                                       511
      <210> 618
      <211> 511
      <212> DNA
      <213> Homo sapien
      <400> 618
acgaggccac agaggcggcg gagagatggc cttcagcggt tcccaggctc cctacctgag
                                                                       60
                                                                       120
tecagetgte ecetttetg ggaetattea aggaggtete caggaeggae tteagateae
tgtcaatggg accgttctca gctccagtgg aaccaggttt gctgtgaact ttcagactgg
                                                                      180
cttcagtgga aatgacattg ccttccactt caaccctcgg tttgaagatg gagggtacgt
                                                                      240
ggtgtgcaac acgaggcaga acggaagctg ggggcccgag gagaggaaga cacacatgcc
                                                                      300
tttccagaag gggatgccct ttgacctctg cttcctggtg cagagctcag atttcaaggt
                                                                      360
gatggtgaac gggatcctct tcgtgcagta cttccaccgc gtgcccttcc accgtgtgga
                                                                       420
caccatctcc gtcaatggct ctgtgcagct gtcctacatc agettccagc ctcccggcgt
                                                                       480
gtggcctgcc aacccggctc ccattaccca g
                                                                       511
      <210> 619
      <211> 413
      <212> DNA
      <213> Homo sapien
      <400> 619
gaatteggea egagetggae aggagaagag cetggetget gaaggeaggg etgaeaegae
                                                                       60
cacgggcagc attgctggag ccccagagga tgaaagatcg cagagcacag ccccccaggc
                                                                      120
accagagtgc ttcgaccetg ceggaceggc tgggctcgtg aggccgacat ctggcctttc
                                                                      180
ccagggccca ggaaaggaaa ccttggaaag tgctctaatc gctctagact ctgaaaaacc
                                                                      240
caagaaactt cgcttccacc caaagcagct qtacttctct gccaggcagg gtgagctgca
                                                                      300
gaaggtgett ctcatgctgg ttgatggaat tgatcccaac ttcaaaatgg agcaccaaag
                                                                      360
taagegttee ceattacatg etgetgegga ggetggeeae gtggaeatet gee
                                                                       413
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the second of th

<213> Homo sapien

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                                                                       120
aaaaaaactcc tggtgccagg aaaaattcag cacattctct gcacaggaaa cctttgcacc
                                                                       180
aaagagagtt atgactatct caagactctg gctggtgatg ttcatattgt gagaggagac
                                                                       240
ttcgatgaga atctgaatta tccagaacag aaagttgtga ctgttggaca gttcaaaatt
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ggtctgatcc atggacatca agttattcca tggggagata tggccagctt agccctgttg
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                                                                       120
totagottgc aagagogtta otoccottca tagotttaaa aggttttogc actgogtgca
                                                                       180
gttagagtag ctaaatcttg tqtqacqctc cacaaacact tqtaagaatt ttqcaqagaa
                                                                       240
agataaccqt tgccaccaa tgcccccac aggcattcta ctccccaqta cctcttaqqq
                                                                       300
tgggagaaat ggtgaagagt tgttcctaca acttgctaac ctagtggaca gggtagtaga
                                                                       360
ttagcatcat ccggatagat gtgaagagga cggctgtttg gataataatt aaggataaaa
                                                                       420
                                                                       421
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                                                                       120
caaaattatt tttttctgta aagtataata tataaaactt cttgcttaaa ttgaatttct
                                                                       180
atattagtgg ttaattgcag tttattaaag ggatcattat cagtaatttc atagcaactg
                                                                       240
ttctagtgtt ttgtgttttt aaaacagaat taggaatttg agatatctga ttatattttt
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catatgaatc acagacctcg gccgcgacca cgctaagggc gaattccagc acactggcgg
                                                                       360
ccgctactag tggatccgag ctcggtacca agcttgggcg taatcatggt catagcctgt
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                                                                       120
aatottocca ttoccagaat ccagaatttt ggaagccatt ttaaccaggg gtattttttn
                                                                       180
caccattacc ttttggaact ttccaaatta atggcctttt aaaaaggttg gaaggggaaa
                                                                       240
accaaaaggc caaaatttta aaaaggttgg gggggggaac cttaaaaaaa aaaatgggtt
                                                                       300
ttggggccnc cttttttaa aaggccaaaa ntttttggg ttccaattaa aaaaatttcc
                                                                       360
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                                                                       120
cgccaacagc tcctacctgg cccagcacat ccgtatacac tcaggggcta agccctacag
                                                                       180
ttgtaacttc tgtgagaaat ccttccgcca gctctcccac cttcagcagc acacccgaat
                                                                       240
ccacactggt gatagaccat acaaatgtgc acacccaggc tgtgagaaag ccttcacaca
                                                                       300
actotocaat otgoagtoco acagacggoa acacaacaaa gataaaccot toaagtgoca
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caactgtcat egggegtaca eggatgcage etcaetagag gtgcacetgt etaeqeacae
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                                                                       421
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                                                                        60
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                                                                       120
cccggccccg cgtcgtctgg cgccgccgcc gccagcgcgc atgcaqcaqa ttggaataaa
                                                                       180
tatgatgacc gattgatgaa agcagcagaa aggggggatg tagaaaaagt gacgtcaatc
                                                                       240
cttgctaaaa agggggtcaa tccaggcaaa ctagatgtgg aaggcagatc tgtcttccat
                                                                       300
gttgtgacct caaaggggaa tcttgagtgt ttgaatgcca tccttataca tggagttgat
                                                                       360
attacaacca gtgacactgc agggagaaat gctcttcacc tggctgctaa gtatggacat
                                                                       420
                                                                       421
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      <211> 476
      <212> DNA
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      <400> 626
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                                                                       120
agttatacaa tcttgacaaa gaagaataaa gtgggaagaa tctatttgat tttaaggctt
                                                                       180
accatgtaac tacagtcatc aagagagtgt ggtatcggca gacggtcaga catacagatc
                                                                       240
aatggaatgt aacagaggac ccagaaatag gcccacacag atatgctcaa tggatatttg
                                                                       300
acaagcgtgc aaaacaattc aatggaagaa taagctttca aaaaaatggc gttqqaqcaa
                                                                       360
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476
60
120 180 240 300 360 420 480 503
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1122

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                5
                                  10
Thr Val Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro
           20
                               25
Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln
                           40
Thr Tyr Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu
                       55
Met Val Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys
                   70
Lys Val Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys
                                  90
Phe Ile Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser
           100
                               105
Pro Asp Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu
                           120
                                              125
Thr Val Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr
                       135
                                         140
Tyr Glu Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala
                  150
                                      155
Leu Arg Leu Ile Gln Ser Glu Leu
               165
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                                                                    60
actotaggee acgatgeege agtaccagae etgggaggag tteageegeg etgeegagaa
                                                                   120
getttacete getgaceeta tgaaggeaeg tgtggttete aaatatagge attetgatgg
                                                                   180
gaacttgtgt gttaaagtaa cagatgattt agtttgtttg gtgtataaaa cagaccaagc
                                                                   240
tcaagatgta aagaaaattg agaaattcca cagtcaacta atgcnactta tggtacccaa
                                                                   300
360
tacttaggaa gtaaatatct tttgaattan aaaaagtgtt gg
                                                                    402
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     <213> Homo sapien
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<400> 633	
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<210> 634 <211> 386 <212> DNA <213> Homo sapien	
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cagatggctc cccagccctg aaacagatcg aaatcaacac catctctgcc agctttgggg
                                                                      300
gcctggcctc ccggacccca nctgtgcacc gacatgttct cagtgtcctq agtaaqacca
                                                                      360
aagaagctgg caagatcctc tctaataatc ccagcaaggg act
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                                                                      120
aaaaagaaaa totgacaaat gaattacaaa aagagcaaga gogaatatot gaattagaaa
                                                                      180
taataaattc atcatttgaa aatattttgc aagaaaaaga gcaagagaaa gtacagatga
                                                                      240
aagaaaaatc aagcactgcc atggagatgc ttcaaacaca attaaaagag ctcaatgaga
                                                                      300
gagtggcagc cctgcataat gaccaagaag cctgtaaggc caaaqagcag aatcttagta
                                                                      360
gtcaagtaga gtgtcttgaa cttgagaagg ctcagttgct acaaggcctt gatgaggcca
                                                                      420
aaaataatta tattgtttgc a
                                                                      441
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      <212> DNA
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      <221> misc feature
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                                                                       60
toccgattcc ttttggttcc aagtccaata tggcaactct aaaggatcag ctgatttata
                                                                      120
atcttctaaa ggaagaacag accccccaga ataagattac aqttqttqqq qttqqtqctq
                                                                      180
ttggcatggc ctgtgccatc agtatcttaa tgaaggactt ggcagatgaa cttgctcttg
                                                                      240
ttgatgtcat cgaagacaaa ttgaagggag agatgatgga tctccaacat ggcagccttt
                                                                      300
tcttagaaca ccaaagattg tctntggcaa agactataat gtaactgcaa ctncagctgg.
                                                                      360
cattatcacg ntggggacgt cagaagaagg agaaagccgc ttat
                                                                      404
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     <221> misc feature
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                                                                       60
cagecttage tteggetece ggettgggtg gegeggeegt gecetegttt tggeeteega
                                                                      120
acgcggctcg aatggcaagc caaaattcct tccggataga atatgatacc tttggtgaac
                                                                      180
taaaggtgcc aaatgataag tattatggcg cccagaccgt gagatctacg atgaacttta
                                                                      240
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agattggagg tgtgacagaa cgcatgccaa ccccagttat taaagctttt ggcatcttga aacgagcggc cgctgaagta aaccaggatt atggtcttga tccaaaaatt gctaatgcaa taatgaangc agcanatgaa gnanctgaag gtaaataaaa tgat	300 360 404
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                                                                        60
atccagaaat tagtcatatg ttgaataatc cagatataat gagacaaacg ttggaacttg
                                                                       120
ccaggaatcc acaatgatgc agganaagat gaagaaccaa gacccaactt tnancaacct
                                                                       180
aaaaannntt ccnaggggnn ttnanngttt nanggnentt nteeccaant tttnaggane
                                                                       240
cattgttnat ngntgnncaa aannagttng gnggaaatcc ttttgtttcc ttgggganca
                                                                       300
atacateett tggngaaggt agteaacett ceegtneana aattagaaat ceeetneeca
                                                                       360
atcontgggn tocacaaact toccaaagtt antnagttto cac
                                                                       403
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tatgtgaagc gatttcagta gaatcactta ctcatcctaa aagaaaacat tattccnant
                                                                       120
                                                                       180
accentecttn nnattnecnt nttntaannn aaacntanng ntnnntgnnt gttnannggn
atnancttta aanntgcant ntnntttant cctccaaatn tttttcggtt tcntntgaga
                                                                       240
                                                                       300
ancaccanaa netttette cettntette agtanttgea anagganace teenttnagg
actggcntag ngaacgtaat ccatgcttta actgccatta aacagcccca tggttggatt
                                                                       360
ttttttttt ttngagtngg ctttccaaaa ccttgtcaaa aac
                                                                       403
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                                                                        60
acaacettte cctggtggtg cacggaccgg gggacttgcg cctggagaac tatectatec
                                                                       120
ctgaaccagg cccaaatgag gtcttgctga ggatgcattc tgttggaatc ttgtggctta
                                                                       180
aatgtcacta ctgggagtat gggcnaattg ggaattttat tgngaaaaac ccatggggtt
                                                                       240
ggacatgaag ttcggacagt cnaaaaagtg ggatcatcgg naaagaccta aaaccaggtg
                                                                       300
ateggttgca tcacctgggc tcccgaaaaa tgataattnt gaagatggcc atacatntgt
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accttcatnt tttntggcac ccccccnata cggaactttg cggtt
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                                                                       120
ccggagggac tgcaaaagct ctcagggatg ctggtctggc agtcagagat gtctctgagt
                                                                       180
tgacgggatt tcctgaaatg ttggggggac gtgtgaaaac tttgcatcct gcagtccatg
                                                                       240
ctggaatcct agctcgtaat attccagaag ataatgctga catggccaga cttgatttca
                                                                       300
atcttataag agttgttgcc tgcaatctct atccctttgt aaagacaagt ggcttctcca
                                                                       360
ggtgtaactg ttgaggangc tgtgggagca aattgacatt ggtgggagta ac
                                                                       412
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ngntctgntc ggctgattnc cagctatgan acaaggagaa tgaaaatatg aagaaaaagc
                                                                       120
tgaacaaaaa agttanntag ctaaaacagg acttgcagnn ttnaaaacag gtccttgatg
                                                                       180
gcaaagaaga ggttgagaaa caacntagag aaaatattna aantctaaat tccatggtag
                                                                       240
aacgccaaga gaaagatett ggeegtette aggtagacat ggatgaaett gaagaaaaga
                                                                       300
accgaagtat tcangctgcc tggatagtgc atacaaagaa cttactgatc tttacaaagc
                                                                       360
caatgctgca aangatagtg aggnacanga agctgctctn accgtgaaat ga
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                                                                        60
eggetetgee eggetgeege eeggeatgaa cateatggat tteaacgtga agaaacttgg
                                                                       120
cgggccgacc gggcaccttt tcttaagccg gcccgtgnaa tttanaaaaa aaaaacttgg
                                                                       180
ncaagcaaaa aaaaanaaaa ttggncctta ncttgaaaan cttcttaaca aaacttaatg
                                                                       240
gtccaaaata ttgaccgaaa aaaaaatgna ncaaaccnna ntgnttttgc acccaatncn
                                                                       300
aatnoonnga nnaaaaaaat tgnttattaa aaacntgaat aaaaancccc aannotatna
                                                                       360
acaaccccga actttttgga cnatntntna ntgatnnnng aacntaattt ggc
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      <210> 649
      <211> 409
      <212> DNA
      <213> Homo sapien
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                                                                       120
actggtgctt ggaactgcta ttgttgaggc tcatgatgga catgatgatg atgtgattga
                                                                       180
tattgaggat gaccttgacg atgtcattga agaggtagaa gactcaaaac cagataccac
                                                                       240
tgctcctcct tcatctccca aggttactta caaagctcca nttccaacag gggaagtata
                                                                       300
ttttgctgat tcttttgaca gaggaactct gtcagggtgg attttatnca nagccaanaa
                                                                       360
agacnatccn atgatgaaaa ttgccnaata tnatggaaaa gtgggaggt
                                                                       409
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      <211> 413
      <212> DNA
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     <223> n = A, T, C \text{ or } G
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                                                                       120
aagaaggtga taaccatgtt tgtacagcga caggtgtttg ctgagaacaa ggatgagatt
                                                                       180
gctttagtcc tgtttggtac agatggcact gacaatcccc tttctggtgg ggatcagtat
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cagaacatca cagtgcacag acatctgatg ctaccagatt ttgatttgct ggaggacatt
                                                                       300
gaaagcaaaa tocaaccagg ttotcaacag gotgacttoo tggatgcact aatogtgago
                                                                       360
atggatgtga ttcacatgaa acaataggaa agaagtttga gaanaagcat att
                                                                       413
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      <211> 441
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     <223> n = A, T, C or G
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                                                                       120
teccaetgag catgeagace tgeagggaag aactgeaett caegatgeeg caatggeaga
                                                                       180
ttgtccttct agcatacage tgctttgtga ccatggggcc tctgtgaatg ccaaagatgt
                                                                       240
agacgggcgg acaccacttg ttctggctac tcagatgagt aggccaacaa tgtqtcaact
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gctgatagat agaggagcgg atgttaattc caqagacaaa caaaacagaa ctgccctcat
                                                                       360
gctaggttgc gaatatggtt gcagagatgc agtagaagtc ttaattaaaa atgggtgctg
                                                                       420
atataagett getggatgeg c
                                                                       441
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     <211> 412
     <212> DNA
     <213> Homo sapien
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<pre><400> 652 gettetetet cetgtgeaaa atggeaacte ttaaggaaaa acteattgea ceagttgegg aagaagagge aacagtteea aacaataaga teaetgtagt gggtgttgga caagttggta tggegtgtge tateageatt etgggaaagt etetggetga tgaaettget ettgggatg ttttggaaga taagettaaa ggagaaatga tggatetgea geatgggage ttatteete agacacetaa aattgtggea gataaagatt attetgtgae egeeaattet aagattgtag tggtaaetge aggagteeg teageaagaa ggggagagte ggeteaatet ggtgeagaga aatggtaatg tetteaaatt eattateet eagateegea agtaeagtee tg</pre>	60 120 180 240 300 360 412
<210> 653 <211> 414 <212> DNA <213> Homo sapien	
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<210> 654 <211> 404 <212> DNA <213> Homo sapien	
<pre><400> 654 gcatggcgga gctgacggtg gaggttcgcg gctccaacgg ggctttctac aagggattta tcaaagatgt ccacgaagac tccctcacag ttgtttttga aaataattgg caaccagaac gccaggttcc gtttaatgaa gtgcgattac caccaccacc tgatataaaa aaagaaatta gtgaaggaga tgaagtagag gtatattcaa gagcaaatga ccaagagcca tgtggatggt ggctggctaa agttcggatg atgaaaggcg agttttatgt cattgaatat gctgcttgtg atgccactta caatgaaata gtcacatttg aacgacttcg gcctgtcaat caaaataaaa ctgtcaaaaa aaataccttc tttaagtgca cagtggatgt tcct</pre>	60 120 180 240 300 360 404
<210> 655 <211> 402 <212> DNA <213> Homo sapien	
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<210> 656 <211> 416 <212> DNA <213> Homo sapien <400> 656	

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<210> 657 <211> 402 <212> DNA <213> Homo sap	ien				
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<210> 658 <211> 404 <212> DNA <213> Homo sap	ien				
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      <211> 411
      <212> DNA
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                                                                       120
gaacgcatet cagecegagg tgetggteee cateegetgg acatggagat egatggeag
                                                                       180
aagctgcgag acgccttcac ctggaacatg aatgagaagt tgatgacgcc tgagatgttt
                                                                       240
tcagaaatcc tctgtgacga tctggatttg aacccgctga cgtttgtgcc agccatcgcc
                                                                       300
tetgecatea gacageagat egagteetae eecaeggaca geateetgga ggaceagtea
                                                                       360
gaccagegeg teateateaa getgaacate catgtgggaa acattteeet q
                                                                       411
      <210> 665
      <211> 409
      <212> DNA
      <213> Homo sapien
      <400> 665
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catgacttcc tacagetate gecagtegte ggecacgteg teetteggag geetgggegg
                                                                       120
cggctccgtg cgttttgggc cgggggtcgc ttttcgcgcg cccagcattc acgggggctc
                                                                       180
eggeggeege ggegtateeg tgteeteege eegetttgtg teetegteet eetegggggg
                                                                       240
ctacggcggc ggctacggcg gcgtcctgac cgcgtccgac gggctgctgg cgggcaacga
                                                                       300
gaagctaacc atgcagaacc tcaacgaccg cctggcctcc tacctggaca aggtgcgcgc
                                                                       360
cctggaggcg gccaacggcg agctagaggt gaagatccgc gactggtac
                                                                       409
      <210> 666
      <211> 411
      <212> DNA
      <213> Homo sapien
      <400> 666
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tgctgctgct gccaggaatt ccaggttgga ggggcggcaa cctcctgcca gccttcaggc
                                                                       120
cactctcctg tgcctgccag aagagacaga gcttgaggag agcttgagga gagcaggaaa
                                                                       180
gcagcctccc ccgttgcccc tctggatcca ctgcttaaat acggacgagg acagggcct
                                                                       240
gtetecteag etteaggeae caccactgae etgggaeagt gaategaeaa tgeegtette
                                                                       300
tgtctcgtgg ggcatcctcc tgctggcagg cctgtgctgc ctggtccctg tctccctggc
                                                                       360
tgaggatccc cagggagatg ctgcccagaa gacagataca tcccaccatg a
                                                                       411
      <210> 667
      <211> 412
      <212> DNA
     <213> Homo sapien
     <400> 667
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                                                                        60
caagacagag aacagttaat tcagaagctt aattgtgaaa aagatgaagc tattcagact
                                                                       120
gccctaaaag aatttaaatt ggagagagaa gttgttgaga aagagttatt agaaaaagtt
                                                                       180
aaacatcttg agaatcaaat agcaaaaagt cctgccattg actctaccag aggagattct
                                                                       240
tcaagcttag ttgctgaact tcaagaaaag cttcaggaag aaaaagctaa gtttctagaa
                                                                       300
caacttgaag agcaagaaaa aagaaagaat gaagaaatgc aaaatqttcq aacatctttg
                                                                       360
attgcggaac aacagaccaa ttttaacact gttttaacaa gagagaaaat ga
                                                                       412
      <210> 668
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<211> 000 <211> 411.

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      <213> Homo sapien
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      <221> misc feature
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      <223> n = A, T, C or G
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                                                                        60
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cttccncctg ncacccgggg agtannnntt aattgtgaan aagatgaaag ctattcagac
ttgncctnnn ataatttnaa ttggngagga gaanntnttn tnatcaaaag ttnttttana
                                                                       180
aaaagntann ncatcttnnn ntaatnaaag tattacanna ntnactgccn attgacttta
                                                                       240
ccanaagaga angcttcnng gctttgttgc tgaancttaa tnaaaaggnt atggggantn
                                                                       300
nanaaaannt aanttnnntn ganntaatct ttgnttgcag cttatcatnn ttngntatna
                                                                       360
aannaganaa tanttotaat nnntgtttto gaatotatna tnnotnnttt t
                                                                       411
      <210> 669
      <211> 412
      <212> DNA
      <213> Homo sapien
      <400> 669
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                                                                        60
taatactttg aggaacactg tggaaacaga aagagaggag tccaagattc tactggaaaa
                                                                       120
gatggaactt gaagtggcag agagaaaatt atccttccat aatctgcagg aagaaatgca
                                                                       180
tcatctttta gaacagtttg agcaagcagg ccaagcccag gctgaactag agtctcggta
                                                                       240
tagtgctttg gagcagaagc acaaagcaga aatggaagag aagacctctc atattttgag
                                                                       300
tetteaaaag actggacaag agetgeagte tgeetgtgat getetaaagg atcaaaatte
                                                                       360
aaagcttctc caagataaga atgaacaggc agttcagtca gcccagacca tt
                                                                       412
      <210> 670
      <211> 411
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1)...(411)
      <223> n = A, T, C or G
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acgagagcag ccacccagat ttgcacagcc tggctccttt gagtatgaat atgccatgcg
                                                                       120
ctggaaggca ctcattgaga tggagaagca gcancaggac caagtggacc gcaacatcaa
                                                                       180
ggaggctcgt gagaagctgg agatggagat ggaagctgca cgccatgagc accaggtcat
                                                                       240
gctaatgaga caggatttga tgaggcgcca agaaqaactt cggaggatgg aagaqctgca
                                                                       300
caaccaagag gtgcaaaaac gaaagcaact ggagctcagg caggaggaag ancqcaggcg
                                                                       360
ccgtgaagaa ganatgcggc ggcagcaaga agaaatgatg cggcgacagc a
                                                                       411
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      <211> 411
      <212> DNA
      <213> Homo sapien
      <220>
      <221> misc feature
      <222> (1) ... (411)
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                                                                       120
cgaccccttt gctgatgcaa ctaagggtga cgacttactn ccggcaggga ctgaggatta
                                                                       180
cattcatata agaatccagc aacggaacgg cagaaagaca ctgactactg ttcagggcat
                                                                       240
tgcagatgat tatgacaaaa agaaacttgt gaaagctttc aaaaagaaat ttgcctgtaa
                                                                       300
tggtactgtg attgaacatc ctgaatacgg agaggttatt cagcttcaag gtgaccaaag
                                                                       360
aaaaaacatc tgccagtttc tcttggaggt tggcattgta aaggaggaac a
                                                                       411
     <210> 672
     <211> 409
     <212> DNA
     <213> Homo sapien
     <400> 672
ggcacgaggc ccactccacc ttactaccag acaaccttag ccaaaccatt tacccaaata
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aagtataggc gatagaaatt gaaacctggc gcaatagata tagtaccgca agggaaagat
                                                                       120
                                                                       180
gaaaaattat aaccaagcat aatatagcaa ggactaaccc ctataccttc tgcataatga
                                                                       240
attaactaga aataactttg caaggagagc caaagctaag acccccgaaa ccagacgagc
                                                                       300
tacctaagaa cagctaaaag agcacacccg tctatgtagc aaaatagtgg gaagatttat
aggtagaggc gacaaaccta ccgagcctgg tgatagctgg ttgtccaaga tagaatctta
                                                                       360
gttcaacttt aaatttgccc acagaaccct ctaaatcccc ttgtaaatt
                                                                       409
     <210> 673
     <211> 412
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(412)
     <223> n = A, T, C or G
     <400> 673
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eggegeeget ttetgegace tggeegteag ecceaegteg eeggeetgga ggggeaaaga
                                                                       120
ggacgagggg gccgcggctt cctccgggga ccttggcttg cctggattgc caggagctgg
                                                                       180
aagttgacat tgagtetagg etgaggatgg aaggtgtgga getgaaggaa gaatggeagg
                                                                       240
                                                                       300
atgaagattt tecaataeet ttaeeagaag atgaeageat tgaageagat acaetagatg
gaactgatcc agacagacag cctggctcct tagaagttaa tgggaacaaa gtaaggaaga
                                                                       360
aactgatggc cccagacatc agcetgaccc tggatcetgg tgaagactet et
                                                                       412
     <210> 674
     <211> 413
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
     <222> (1)...(413)
     <223> n = A,T,C or G
     <400> 674
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ccacgccgtt caatgtcgca gaggggaagg aggttcttct actcgcccac aacctgcccc
                                                                       120
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agaatcgtat tggttacagc tggtacaaag gcgaaagagt ggatggcaac agtctaattg

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taggatatgt aatàggaact caacaagcta ccccagggcc cgcatacagt ggtcgagaga
                                                                       240
caatataccc caatgcatcc ctgctgatcc agaacgtcac ccagaatgac acaggattct
                                                                       300
ataccctaca agtcataaag tcagatcttg tgaatgaaga agcaaccgga cagttccatg
                                                                       360
tatacccgga getgcccaag ccctccatct ncagcaacaa ctccaacccc qtg
                                                                       413
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     <211> 411
     <212> DNA
     <213> Homo sapien
     <220>
     <221> misc feature
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     <223> n = A, T, C or G
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agaggatgag gaggaatcct tgaatgaagt aggctatgat gacatcggtg gttgcaggaa
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gcagctaget caaataaagg agatggtgga gctgccactg agacatnetg cgctctttaa
                                                                       180
ggnqattgqt qtaaaqcctc ctcqqqqaat cttqttqtat qqqccttctq qqacaqqqaa
                                                                       240
gaccctgatt gctcgagctg tggcaaatga aactggagcc ttcttctttc tgatcaatgg
                                                                       300
tcctgaaatc attgancaaa ttggctggtg agtctgagag caaccttcgt aaagcctttg
                                                                       360
aggaagctga aaagaatgct nctgctatca tcttcatcga tgaacttgat g
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Arg Trp Arg Gln Leu Val Glu Lys Gly Pro Gln Tyr Gly Thr Val Glu
Lys Ala Trp Met Ala Phe Met Ser Glu Ala Glu Arg Val Ser Glu Leu
His Leu Glu Val Lys Ala Ser Leu Met Asn Asp Asp Phe Glu Lys Ile
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Lys Glu Thr Lys Glu Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro
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Ala Ala Cys Lys Glu Glu Lys Leu Ala Ile Ser Arg Glu Ala Asn Ser
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Ser Val Ser Ser Lys Ile Pro Phe Asp
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	tcaaaggtgg					
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	ccgcagtgga					
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	gcatattccc					
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	tgtatgtctt					
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	ttctcttctg					
	ttaggcctca					
	caattataca					
	ataagtccac					
	gcaagtgcgc					
	caagccatgg					
	gtggaggtga					
	ttccacaaaa					
	ggctgggatc					
	aacctggaca					
	ggagcagccc					
	ccaggaaaca					
	gccctgaccc					
	ctgaaggatt					
	caagagttgg					
	agtctcttgc					
	cgcaagagcc					
	ttcatcgggc					
	ataatcatgt atcaccccag					
	accactgat					
	actggcctct					
	gcagtttgtt					
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<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
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Val	Asn 50	Glu	Leu	Leu	Leu	Gly 55	Met	Ala	Ser	Gln	Ile 60	Ser	Glu	Leu	Glu
Asp 65	Asn	Ile	Val	Val	Glu 70	Asp	Leu	Arg	Asp	Tyr 75	Trp	Pro	Gly	Pro	Gly 80
Lys	Phe	Ser	Arg	Thr 85	Asp	Tyr	Val	Ala	Ser 90	Ser	Ile	Gln	Arg	Gly 95	Arg
Asp	Met	Gly	Leu 100	Pro	Ser	Tyr	Ser	Gln 105	Ala	Leu	Leu	Ala	Phe 110	Gly	Leu
Asp	Ile	Pro 115	Arg	Asn	Trp	Ser	Asp 120	Leu	Asn	Pro	Asn	Val 125	Asp	Pro	Gln
Val	Leu 130	Glu	Ala	Thr	Ala	Ala 135	Leu	Tyr	Asņ	Gln	Asp 140	Leu	Ser	Gln	Leu
Glu 145	Leu	Leu	Leu	Gly	Gly 150	Leu	Leu	Glu	Ser	His 155	Gly	Asp	Pro	Gly	Pro 160
Leu	Phe	Ser	Ala	Ile 165	Val	Leu	Asp	Gln	Phe 170	Val	Arg	Leu	Arg	Asp 175	Gly
Asp	Arg	Tyr	Trp 180	Phe	Glu	Asn	Thr	Arg 185	Asn	Gly	Leu	Phe	Ser 190	ГÀЗ	Lys
Glu	Ile	Glu 195	Asp	Ile	Arg	Asn	Thr 200	Thr	Leu	Arg	Asp	Val 205	Leu	Val	Ala
Val	Ile 210	Asn	Ile	Asp	Pro	Ser 215	Ala	Leu	Gln	Pro	Asn 220	Val	Phe	Val	Trp
His 225	Lys	Gly	Ala	Pro	Cys 230	Pro	Gln	Pro	Lys	Gln 235	Leu	Thr	Thr	Asp	Gly 240
Leu	Pro	Gln	Суѕ	Ala 245	Pro	Leu	Thr	Val	Leu 250	Asp	Phe	Phe	Glu	Gly 255	Ser
Ser	Pro	Gly	Phe 260	Ala	Ile	Thr	Ile	Ile 265	Ala	Leu	Суз	Суѕ	Leu 270	Pro	Leu
Val	Ser	Leu 275	Leu	Leu	Ser	Gly	Val 280	Val	Ala	Tyr	Phe	Arg 285	Gly	Arg	Glu
His	Lys 290	Lys	Leu	Gln	Lys	Lys 295	Leu	Lys	Glu	Ser	Val 300	Lys	Lys	Ġlu	Ala
Ala 305	Lys	Asp	Gly	Val	Pro 310	Ala	Met	Glu	Trp	Pro 315	Gly	Pro	Lys	Glu	Arg 320
Ser	Ser	Pro	Ile	Ile 325	Ile	Gln	Leu	Leu	Ser 330	Asp	Arg	Cys	Leu	Gln 335	Val
Leu	Asn	Arg	His	Leu	Thr	Val	Leu	Arg	Val	Val	Gln	Leu	Gln	Pro	Leu

340 345 350 Gln Gln Val Asn Leu Ile Leu Ser Asn Asn Arg Gly Cys Arg Thr Leu 360 Leu Leu Lys Ile Pro Lys Glu Tyr Asp Leu Val Leu Leu Phe Ser Ser 375 Glu Glu Glu Arg Gly Ala Phe Val Gln Gln Leu Trp Asp Phe Cys Val Arg Trp Ala Leu Gly Leu His Val Ala Glu Met Ser Glu Lys Glu Leu 410 Phe Arg Lys Ala Val Thr Lys Gln Gln Arg Glu Arg Ile Leu Glu Ile Phe Phe Arg His Leu Phe Ala Gln Val Leu Asp Ile Asn Gln Ala Asp 440 Ala Gly Thr Leu Pro Leu Asp Ser Ser Gln Lys Val Arg Glu Ala Leu 455 Thr Cys Glu Leu Ser Arg Ala Glu Phe Ala Glu Ser Leu Gly Leu Lys 470 475 Pro Gln Asp Met Phe Val Glu Ser Met Phe Ser Leu Ala Asp Lys Asp 490 Gly Asn Gly Tyr Leu Ser Phe Arg Glu Phe Leu Asp Ile Leu Val Val Phe Met Lys Gly Ser Pro Glu Asp Lys Ser Arg Leu Met Phe Thr Met 520 Tyr Asp Leu Asp Glu Asn Gly Phe Leu Ser Lys Asp Glu Phe Phe Thr Met Met Arg Ser Phe Ile Glu Ile Ser Asn Asn Cys Leu Ser Lys Ala Gln Leu Ala Glu Val Val Glu Ser Met Phe Arg Glu Ser Gly Phe Gln Asp Lys Glu Glu Leu Thr Trp Glu Asp Phe His Phe Met Leu Arg Asp His Asp Ser Glu Leu Arg Phe Thr Gln Leu Cys Val Lys Gly Gly 600 Gly Gly Gly Asn Gly Ile Arg Asp Ile Phe Lys Gln Asn Ile Ser Cys Arg Val Ser Phe Ile Thr Arg Thr Pro Gly Glu Arg Ser His Pro Gln 630 635 Gly Leu Gly Pro Pro Ala Pro Glu Ala Pro Glu Leu Gly Gly Pro Gly 650

Leu Lys Lys Arg Phe Gly Lys Lys Ala Ala Val Pro Thr Pro Arg Leu Tyr Thr Glu Ala Leu Gln Glu Lys Met Gln Arg Gly Phe Leu Ala Gln 680 Lys Leu Gln Gln Tyr Lys Arg Phe Val Glu Asn Tyr Arg Arg His Ile Val Cys Val Ala Ile Phe Ser Ala Ile Cys Val Gly Val Phe Ala Asp Arg Ala Tyr Tyr Gly Phe Ala Leu Pro Pro Ser Asp Ile Ala Gln Thr Thr Leu Val Gly Ile Ile Leu Ser Arg Gly Thr Ala Ala Ser Val Ser Phe Met Phe Ser Tyr Ile Leu Leu Thr Met Cys Arg Asn Leu Ile 760 Thr Phe Leu Arg Glu Thr Phe Leu Asn Arg Tyr Val Pro Phe Asp Ala Ala Val Asp Phe His Arg Trp Ile Ala Met Ala Ala Val Val Leu Ala Ile Leu His Ser Ala Gly His Ala Val Asn Val Tyr Ile Phe Ser Val Ser Pro Leu Ser Leu Leu Ala Cys Ile Phe Pro Asn Val Phe Val Asn 825 Asp Gly Ser Lys Leu Pro Gln Lys Phe Tyr Trp Phe Phe Gln Thr 840 Val Pro Gly Met Thr Gly Val Leu Leu Leu Val Leu Ala Ile Met 855 860 Tyr Val Phe Ala Ser His His Phe Arg Arg Arg Ser Phe Arg Gly Phe 870 Trp Leu Thr His His Leu Tyr Ile Leu Leu Tyr Ala Leu Leu Ile Ile 890 His Gly Ser Tyr Ala Leu Ile Gln Leu Pro Thr Phe His Ile Tyr Phe Leu Val Pro Ala Ile Ile Tyr Gly Gly Asp Lys Leu Val Ser Leu Ser Arg Lys Lys Val Glu Ile Ser Val Val Lys Ala Glu Leu Leu Pro Ser Gly Val Thr Tyr Leu Gln Phe Gln Arg Pro Gln Gly Phe Glu Tyr Lys

199

Ser Gly Gln Trp Val Arg Ile Ala Cys Leu Ala Leu Gly Thr Thr Glu 965 970 975

Tyr His Pro Phe Thr Leu Thr Ser Ala Pro His Glu Asp Thr Leu Ser 980 985 990

Leu His Ile Arg Ala Val Gly Pro Trp Thr Thr Arg Leu Arg Glu Ile 995 1000 1005

Tyr Ser Ser Pro Lys Gly Asn Gly Cys Ala Gly Tyr Pro Lys Leu Tyr 1010 1015 1020

Leu Asp Gly Pro Phe Gly Glu Gly His Gln Glu Trp His Lys Phe Glu 1025 1030 1035 1040

Val Ser Val Leu Val Gly Gly Gly Ile Gly Val Thr Pro Phe Ala Ser 1045 1050 1055

Ile Leu Lys Asp Leu Val Phe Lys Ser Ser Leu Gly Ser Gln Met Leu 1060 1065 1070

Cys Lys Ile Tyr Phe Ile Trp Val Thr Arg Thr Gln Arg Gln Phe 1075 1080 1085

Glu Trp Leu Ala Asp Ile Ile Gln Glu Val Glu Glu Asn Asp His Gln 1090 1095 1100

Asp Leu Val Ser Val His Ile Tyr Val Thr Gln Leu Ala Glu Lys Phe 1105 1110 1115 1120

Asp Leu Arg Thr Thr Met Leu Tyr Ile Cys Glu Arg His Phe Gln Lys 1125 1130 1135

Val Leu Asn Arg Ser Leu Phe Thr Gly Leu Arg Ser Ile Thr His Phe 1140 1145 1150

Gly Arg Pro Pro Phe Glu Pro Phe Phe Asn Ser Leu Gln Glu Val His 1155 1160 1165

Pro Gln Val Arg Lys Ile Gly Val Phe Ser Cys Gly Pro Pro Gly Met 1170 1175 1180

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Ala His Phe Met His His Tyr Glu Asn Phe 1205 1210

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<211> 277

<212> PRT

<213> Homo sapiens

<400> 693

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Thr Ser Leu Ser Pro Arg Ser Glu Met Arg Ala Asp Asp Lys Phe Val 35 40 45

Asn Val Thr Ile Val Thr Ile Leu Ala Glu Thr Thr Ser Asp Asn Glu 50 55 60

Lys Thr Val Thr Glu Lys Ile Asn Lys Ala Ile Arg Ser Ser Ser Ser 65 70 75 80

Asn Phe Leu Asn Tyr Asp Leu Thr Leu Arg Cys Asp Tyr Tyr Gly Cys
85 90 95

Asn Gln Thr Ala Asp Asp Cys Leu Asn Gly Leu Ala Cys Asp Cys Lys
100 105 110

Ser Asp Leu Gln Arg Pro Asn Pro Gln Ser Pro Phe Cys Val Ala Ser 115 120 125

Ser Leu Lys Cys Pro Asp Ala Cys Asn Ala Gln His Lys Gln Cys Leu 130 135 140

Ile Lys Lys Ser Gly Gly Ala Pro Glu Cys Ala Cys Val Pro Gly Tyr 145 150 155 160

Gln Glu Asp Ala Asn Gly Asn Cys Gln Lys Cys Ala Phe Gly Tyr Ser 165 170 175

Gly Leu Asp Cys Lys Asp Lys Phe Gln Leu Ile Leu Thr Ile Val Gly
180 185 190

Thr Ile Ala Gly Ile Val Ile Leu Ser Met Ile Ile Ala Leu Ile Val 195 200 205

Thr Ala Arg Ser Asn Asn Lys Thr Lys His Ile Glu Glu Glu Asn Leu 210 215 220

Ile Asp Glu Asp Phe Gln Asn Leu Lys Leu Arg Ser Thr Gly Phe Thr 225 230 235 240

Asn Leu Gly Ala Glu Gly Ser Val Phe Pro Lys Val Arg Ile Thr Ala 245 250 255

Ser Arg Asp Ser Gln Met Gln Asn Pro Tyr Ser Arg His Ser Ser Met 260 265 270

Pro Arg Pro Asp Tyr 275

<210> 694

<211> 157

<212> DNA

<213> Homo sapien

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<212> DNA
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tggttaagta atccactgag gacctgaagg ggaaaatgga cttacctttc tcatatactt
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ggcctggcta ggacactggg tgccagacag ccttctgagg ggattttctt tctaaatgag
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<210> 696
<211> 188
<212> DNA
<213> Homo sapien
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                                                                        120
cctgcccca ggctgctaca atacccaggc tcttgagcaa cagtnaagct gccataaata
                                                                        180
tttctcaa
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<210> 697
<211> 289
<212> DNA
<213> Homo sapien
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<221> misc_feature
<222> (1) ... (289)
<223> n = A, T, C or G
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                                                                        120
gtgctaagtg ggaattgatt ataaacttga attetteeat caacaaatat ctacctetee
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tgtccagctt gcctcagatc ttcaggntct ctcttctctg aggcagctaa gcttctacat
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<210> 698
<211> 193
<212> DNA
<213> Homo sapien
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<221> misc feature
<222> (1) ... (193)
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                                                                       120
actaaggcta accaaactta gatataaatc ctaccaataa aatttttcag ntttaagttt
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tacagtttga ttt
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<210> 699
<211> 279
<212> DNA
<213> Homo sapien
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<221> misc_feature
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tccagnggga taccetectt gtettgaatt ttggetttga cattetcaat ggtgtcactg
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ggctcgacct caagggtgat ggttttgcca gtgagggtct tcacaaagat ctgcatgttt
                                                                       240
gcgtccgcac gaccgccgcc accaaccagc tcggccgcc
                                                                       279
<210> 700
<211> 340
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(340)
<223> n = A, T, C or G
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gtectetatg geccagaega ecceaceatt teceecteat acacetatta ecgnecaggg
                                                                       180
gtgaacctca gcctctcctg ccatgcagcc tctaacccac ctgcacagta ttcttggctg
                                                                       240
attgatggga acatccagca acacacaca gagctcttta tctccaacat cactgagaag
                                                                       300
aacagcggac tctatacctg ccaggccaat aactcagcca
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<210> 701
<211> 277
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (277)
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gcaggtgggt tagaggctgc atggcaggag aggctgaggt tcacccctgg acggtaatag
                                                                       180
gngtatgagg gggaaatggt ggggtegtet gggccataga ggacattcag gatgactggg
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```

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277
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<210> 702
<211> 255
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A, T, C or G
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                                                                        180
aaattetaca agggcaagaa gtacaageee etggaeetge ggeetaagaa gacaegtgee
                                                                        240
atgegeegee ggeteaacaa geaegaggag aacetgaaga ceaagaagea geageggaag
gagcggctgt acccg
                                                                        255
<210> 703
<211> 224
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(224)
<223> n = A, T, C or G
·<400> 703
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agggagcaca gtctgcaccc agctctcatc ccatcggagc tgctgcgact cccgcaggnt
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cttccggaac tggtttagct tgcccgcagn atcagnaaag tttg
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<210> 704
<211> 445
<212> DNA
<213> Homo sapien
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<221> misc feature
<222> (1)...(445)
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gaatctggac aattttttga taaactttaa ggctgctaaa taatttacag aaactgtgaa
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                                                                        240 -
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tttgaaatgg ntatcctaaa gaatttcctt aaattcagat tttgcaaaat tcctactctc
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caagtcatca agngaacact aaaagcaact ttactcgtga atacagggga ctctttacga
                                                                        360
ggcatgcatt tttcataaat ctaggccaaa gngaactaat tgagatttaa ttctaaattc
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<210> 705
<211> 107
<212> DNA
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<220>
<221> misc feature
<222> (1) ... (107)
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tnagaacctn aattagccat ttgccatctt nagagagtct tnnccat
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<210> 706
<211> 113
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(113)
<223> n = A, T, C or G
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ttggggggat gctttcactg cttcacttcc tttctatgac agctnaggga atc
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<210> 707
<211> 283
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(283)
<223> n = A, T, C or G
<400> 707
ctgctccaag gccatcaaga tcttcatggg gaggacggag ctgaagntgg aagacaagca
                                                                         60
ccgtgtggtg atccagcgtg atgagggtca ccacgtggcc tacaccacgc gggaggtggg
                                                                        120
ccagtanctg gnggnggagt ccagcacggg catcatcgnc atctgggaca agaggaccac
                                                                        180
cgtgttcatc aagctggctc cctcctanaa gggcaccgtg ngnggcctgt gtgggnactt
                                                                        240
tgaccaccgc tccaacaacg acttcaccac gcgggnccac atg
                                                                        283
<210> 708
<211> 341
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(341)
<223> n = A,T,C or G
<400> 708
ctgtccaatg acaacaggac cctcactcta ctcagtgtca caaggaatga tgtaggaccc
                                                                         60
tatgagtgtg gaatccagaa caaattaagt gttgaccaca gcgacccagt catcctgaat
                                                                        120
gtcctctatg gcccagacga ccccaccatt tccccctcat acacctatta ccgtccaggg
                                                                        180
gngaacctca gcctctcctg ccatgcagcc tctaacccac ctgcacagta ttcttggctg
                                                                        240
attgatggga acatccagca acacacaca gagctcttta tctccaacat cactgagaag
                                                                        300
```

```
aacageggac tetatacetg ceaggecaat aacteageca g
                                                                       341
<210> 709
<211> 376
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (376)
<223> n = A, T, C or G
<400> 709
ccaagtccag gggcgtggag gccgcccggg agcggatgtt caatggtgag aagatcaact
                                                                        60
anaccgaggg tcgagccgtg ctgcacgtgg ctctgcggaa ccggtcaaan acacnnatcc
                                                                       120
tggtagacgg caaggatgtg atgccagagg tcaanaaggt tctgganaag atgaagtctt.
                                                                       180
tetgccageg tgtccggage ggngactgga aggggtanac aggcaagace atcacggacg
                                                                        240
tcatcaacat tggcattggc ggctccgacc tgggacccct catggngact gaagccctta
                                                                        300
agtcatactc ttcaggaggn ccccgcgnct gggatgnctc caacattgat ggaactcaca
                                                                       360
ttgccaaaac cctggc
                                                                       376
<210> 710
<211> 232
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A, T, C or G
<400> 710
ctgctgtata ttcagcattg tgggaggagc tgtgaaagac anagaacagt anagggtgtg
                                                                         60
gnccctgccc tcgagaggnt tanagtctag gtggagaaac gggaancagg acacatgggg
                                                                        120
agccgagaga aaanagtcca ggccagtatg ttacaggagc tggaaggtgt ttggggtcag
                                                                       180
accccaatac tccaagtaca ctaagcactt cagtgcctcc aggggctcaa cg
                                                                       232
<210> 711
<211> 317
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (317)
<223> n = A,T,C or G
<400> 711
caggtaaaat agatttaatt taggaaagct cattttatat gagtttccaa ctaattatta
                                                                         60
gagtcagaaa caaagaaaat aaaatcagag aaaatcctct gtagaaaaaa tacacaaaga
                                                                        120
acatttctac atgtgaaaaa acagtaaaca gtgttaacat ccaagttatt agtctcaatt
                                                                        180
ccacgtetec tagtgaacac cactateaac ettgagatet gatttgntet tgteattett
                                                                        240
cactgagtag atgaaatatg ttaaggtgtc tttttcattc actggaatag acctaaagtg
                                                                        300
gcaaccaact atctcaa
                                                                        317
<210> 712
<211> 154
<212> DNA
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<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(154)
<223> n = A, T, C or G
<400> 712
                                                                         60
tntgtagaaa aaatanacaa agaacatttn tanatgtgaa aaaacagtaa acagngttaa
catecaagtt attagtetca attecaegte teetagtgaa caccaetnte aacettgaga
                                                                        120
                                                                        154
tctgatttgn tcttgtcatt cttcactgag taga
<210> 713
<211> 177
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(177)
<223> n = A, T, C or G
<400> 713
ccattcagag gtagaagatg gaggggggc agattctggc agggcagcag agggctctat
                                                                         60
qcacqqqttt caaacctqtt ttccacactc tgtctttgca gntttggtaa ttctgtggtc
                                                                        120
tatttatana gatattaaaa tottgtttat aaaaaaaaaa aaaaaaaaa aaaaaaa
                                                                        177
<210> 714
<211> 216
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (216)
<223> n = A, T, C or G
<400> 714
ctgtgtttcg gctataaaaa ggcggctgaa agaaggggaa aattanttta gacttaattg
                                                                         60
                                                                        120
gaagtttcat atggcacaca ttaccagnag agaaaaagat ataaacggca ataaatatta
ggctcgattt gagaaactct ccccacctca atgctttctt ttcccttgct atttaagggt
                                                                        180
ctactttgca acccgtgtgn gtgtttgtgt gtgtgt
                                                                        216
<210> 715
<211> 376
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(376)
<223> n = A, T, C or G
<400> 715
ctgtgcgagt gtaccggatg cttccacctc tcaccaagaa ccagagaaaa gaaagaaagt
                                                                         60
cgaagtccag ccgagatgct aagagcaagg ccaagaggaa gtcatgtggg gattccagcc
                                                                        120
ctgatacctt ctctgatgga ctcagcagct ccactctgcc tgatgaccac agcagctaca
                                                                        180
                                                                        240
cagttccagg ctacatgcag gacttggagg nggagcaggc cctgactcca gctacaacag
```

atgaggatga ggaagggaaa ggcagccaac aagcgtggat cctctgtcta tggaga					300 360 376
<210> 716 <211> 96 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(96) <223> n = A,T,C or G					
<400> 716 aaacttttta tttgcatatt aaaaaaaaat ggcnctntga			taattaaaat	catttgaana	60 96
<210> 717 <211> 366 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(366) <223> n = A,T,C or G					
<pre><400> 717 gatggaaagg atacagatga agtatcatac tggatgccat gcaaaagatc gagatcctga cagaatcaga gtggtgaaca gagtcttctg aggaaaattc gacaatgctg caagcatttc actaca</pre>	ccgggaatat aatggaaaat gatttcatca tctaaattct	gaggaggtag gaagaacaac agttctcagg cacccagaat	aagngctcct catcctctga aggntgattt cattatctct	ctctgataaa aaatgattct ggntgatcaa agcagatatg	60 120 180 240 300 360 366
<210> 718 <211> 200 <212> DNA <213> Homo sapien		·	•		
<220> <221> misc_feature <222> (1)(200) <223> n = A,T,C or G		·			
<400> 718 aaacatctca catatanaaa gcttctgtgg aaccatggaa tgaagaagat ttgggcaaat aatgctaaat caaattttt	gaagatgaaa	atgagactgg	caaagaacaa	atgctgaatc	60 120 180 200
<210> 719 <211> 336 <212> DNA <213> Homo sapien					

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<220>
<221> misc feature
<222> (1)...(336)
<223> n = A, T, C or G
<400>. 719
ctgtctcaca ctttgcaagc tgtgagagac acatcagagc cctgggcact gtcactgctt
                                                                         60
gcagcctgag ngtaactccc tccttttcta tctgagctct tcctcctcca catcacggca
                                                                        120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatgcccacg
                                                                       180
atggggatgg tgggctggga agacagctcc catctcaggg tgaggggctt gggcagaccc
                                                                        240
teatgetgea catggeaggn gtatetetge teeteteeag aaggeaceae cacageegee
                                                                        300
cacttetgga aggntecate ecettgeagg cettgg
                                                                        336
<210> 720
<211> 167
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (167)
<223> n = A,T,C or G
<400> 720
ggagagtgct agtgaggcgg ccaagaagta natggaggag aatgannagc tcaagaaggg
                                                                        60
agctgctgtt gacggaggca agttggatgt cgggaatgct gaggtgaagt tggaggaaga
                                                                       120
gaacaggagc ctgaaggctg acctgcagaa gctaaaggac gagctgg
                                                                        167
<210> 721
<211> 134
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (134)
<223> n = A, T, C or G
<400> 721
cctagtatga ggagcgttat ggagtggaag tgaaatcana tggctaggcc ggaggncatt
                                                                         60
aggagggctg agagggcccc tgttaggggt catgggctgg gntttacgtg cgtgaggagg
                                                                        120
ggcggagctt gcag
                                                                       134
<210> 722
<211> 353
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(353)
<223> n = A,T,C or G
<400> 722
aaaaatatat acaactatga tgttcaaata tgtattctga gccattatgt tcaaacataa
                                                                         60
atatctggga aattcaaact gctgcaacaa gttaggaaag gattaaggaa aaatgatgag
                                                                       120
ctacaaatta tgtagttgga ggaagaaaaa aatgttactt agcatttatg tctggatagg
                                                                       180
tatgtatttt ctaatttaca tacacatatc cagntgagta tagacaacca tcaaaatgta
                                                                       240
```

accagttaca cagagactag atttcaaaaa ttttaatatc					300 353
<210> 723 <211> 268 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(268) <223> n = A,T,C or G					
<400> 723 ctgagaagag cgccaggaag acacggngtg caccacctcc tggnctggga gcccatagcg agatcttgcc cgtcgccttg ncagggactc aatcatcttg	ttgcgtttct tcgtagtcgc tcgatggnga	ggagctcccc gggcgngtgt	atctgggcac gaaggagcgg	tgcacgaact cccaacttgg	60 120 180 240 268
<210> 724 <211> 344 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(344) <223> n = A,T,C or G				·	
<400> 724 aaagaatcag caaaatttca agncccatga aattaattat cagttagttc attaaagttt ttcaagagta naggtcagag tgccagactg gagtgcagtg aagcgattct cctgcctcag	tttctctgct tggaaattct ncttctttc gtgcgatctg	cgatcttggt cagacagtgc ttttcttttt ggctcactgc	ggacagtttc agtggtatca gagatggagt aatctccacc	atgaagctgt gaaacttgta cttgctctgt	60 120 180 240 300 344
<210> 725 <211> 345 <212> DNA <213> Homo sapien	•				
<220> <221> misc_feature <222> (1)(345) <223> n = A,T,C or G					
<400> 725 aaacaagaga aagtagacag gacacagtgt actctctgag tgcactacta cacaggggcc tttctttttt cccacagagc gggataaaaa tgaacttcga caaggnattt ccccccaaat	cccaatatan tagcaccctc tcggggggtt acagaaaggg	agagaaagga cagcttccag gattccatac gtagagactc	ggaaaaaagc cagagcgaag agnttttgtt ttttcccatt	tagaatteta ggageaggnt cagacaggaa	60 120 180 240 300 345
<210> 726 <211> 305					

210

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<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(305)
<223> n = A, T, C or G
<400> 726
ttgcctgatg tcagagcccc tccacacatg agcctgctcc ctactgccaa caccgtggcc
                                                                        60
cagacagaga cgctttccga ggaagaggtg aagctcctgc agtcgctgaa gnaagganag
                                                                       120
cagatcgtga ggaaaaaggg cgccgaggtt gggggcatgt ctctcttctt accaagctag
                                                                       180
actggqntgc cttttctaac tattccagcc ctacagggcg aggggccata atggagtatc
                                                                       240
cegececttt agaceceagg cgeteacegg cagggeaaga aggngaaate cageageege-
                                                                       300
                                                                       305
<210> 727
<211> 387
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A, T, C or G
<400> 727
ccaacgaggc atcacctctg acggtgtcag tcatcgatga ccggctcaag gagaagatgg
                                                                        60
tggtggagtt ccgccacatg aggaaccatg cctatgagcc actcgccagc ttcctagact
                                                                       120
tcattactta nagttacatg atcgacaacg ngatcctgct catcacaggc acgctgcacc
                                                                       180
agegetecat egetgagete gtgeceaagt gecacecact aggeagette gageagatgg
                                                                       240
aggeogtgaa cattgctcag acacctgctg agctctacaa tgccattctg gtggacacgc
                                                                       300
                                                                       360
ctcttgcggc ttttttccag gactgcattt cagagcagga ccttaacgag atgaacatcg
agateateeg caacacete tacaagg
                                                                       387
<210> 728
<211> 109
<212> DNA
<213> Homo sapien
<400> 728
                                                                        60
ctgactgaca gccagattgc agatgtggct cgcttttgta accgctaccc taatatcgaa
ctatcttatg aggtggtaga taaggacagc atccgcagtg gcgggccag
                                                                       109
<210> 729
<211> 329
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(329)
<223> n = A, T, C or G
<400> 729
aaagcatagg actatagtca gcatgctaga ctgagaggta aacactgatg caattagaac
                                                                        60
aggtactgat gctgtcagtg tttaacacta tgtttagctg tgtttatgct ataaaagtgc
                                                                       120
```

aatattagac actagctagt actgctgcct catgtaactc caaagaaaac aggatttcat

taagtgcatt gaatgtggct atgccgngca gatttatgtg aagngagaag caaacatttc	gctgctattt				240 300 329
<210> 730 <211> 238 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(238) <223> n = A,T,C or G					
<400> 730 aaaaagtggc agagtgactt atgtagncat tttacttatt ttgattagtg taatcgatta tataattatt ttctttgctg	ttattcatta taaaggatat	gctaactttg ttatcaaatc	tctatgtata cagggattgc	tttctagata attttgaaat	60 120 180 238
<210> 731 <211> 297 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(297) <223> n = A,T,C or G					
<400> 731 aaactgaatt ttttgacctt aattagacta attatttat tggagttatt cactgcaaca cgattttgcc tgtgaatatg ctgcttactt aagnetette	ccccatccca aagcaacaat gngtctgtca	gggtataaac gttgtccatg ttcagggcat	aggaattgtt attcaaaatc agctcactgt	ttgatagtgg taagcagttt aggctagcct	60 120 180 240 297
<210> 732 <211> 370 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(370) <223> n = A,T,C or G	٠.				
<pre><400> 732 ctgtcagtct tcctgaaatg ccagcactcc aatcatgatg agttaggtag ncagacatct tggnatggct acagaaatcc gggtaggcag ggcatggggg tattggaaca cacccgcagc acacatatac</pre>	ccgacagngg ataaatacta atctggaaat gaggggaaca	ccccaattag gtatccgcat tattcaaaag cacaaaaccc	aagntcaaaa gaatgaaaac gacgtggttc ccaagcagag	acaaaaatta accctggctt agggaaaagg gtaaaatgaa	60 120 180 240 300 360 370
<210> 733 <211> 242					

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<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(242)
<223> n = A, T, C or G
<400> 733
cctcctattt attctagcca cctctagcct agccgtttac tcaatcctct gatcagggtg
                                                                         60
agcatcaaac tcaaactacg ccctgatcgg cgcactgcga gcagtagccc aagcaatctc
                                                                        120
atatgaagnc accctagcca tcattctact atcaacatta ctaataagtg gctcctttaa
                                                                        180
cetetecace ettateacaa cacaagaaca ectetgatta eteetgeeat catgaceett
                                                                        240
gg
                                                                        242
<210> 734
<211> 368
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (368)
<223> n = A, T, C or G
<400> 734
cctttcttgt aagtgaagaa aaaggaatgc agcaaagaag agttcgacat tggagtcctt
                                                                         60
agttccatca ggatcccatt cgcagccttt agcatcatgt agaagcaaac tgcacctatg
                                                                        120
gctgagatag gtgcaatgac ctacaagatt ttgngttttc tagctgtcca ggaaaagcca
                                                                        180
tcttcagnct tgctgacagt caaagagcaa gtgaaaccat ttccagccta aactacataa
                                                                        240
aagcagccga accaatgatt aaagacctct aaggctccat aatcatcatt aaatatgccc
                                                                        300
aaactcattg ngacttttta ttttatatac aggattaaaa tcaacattaa atcatcttat
                                                                        360
ttacatgg
                                                                        368
<210> 735
<211> 308
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G
<400> 735
ctgtccaata ggcgtagcta tccggacaga gcacgtttgc agaaggggga ctcttcttcc
                                                                         60
aggtagetga aaggggaaga cetgaegtae tntggttagg ntaggaettg eectegtggn
                                                                        120
ggaaactttt cttaaaaaagt tataaccaac ttttctatta aaagtgggaa ttaggagaga
                                                                        180
aggtaggggt tgggaatcag agagaatggc tttggnctct tgcttgtggg actagcctgg
                                                                        240
cttgggacta aatgccctgc tctgaacacg aagcttagna taaactgatg gatatcccta
                                                                        300
ccttgaaa
                                                                        308
<210> 736
<211> 354
<212> DNA
<213> Homo sapien
<220>
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<221> misc feature
<222> (1)...(354)
<223> n = A, T, C or G
<400> 736
cettetgeta egtagtetae aacagaagga tteaggeaat tacetetgee atgeggngga
                                                                         60
acatgggttc atacaaactc ttcttaaggt aaccctggaa gtcattgaca cagagcattt
                                                                        120
ggaagaactt cttcataaag atgatgatgg agatggctct aagaccaaag aaatgtccaa
                                                                        180
tagcatgaca cctagccaga aggtctggta cagagacttc atgcagctca tcaaccaccc
                                                                        240
caatctcaac acgatggatg agttctgtga acaagtttgg aaaagggacc gaaaacaacg
                                                                        300
teggeaaagg ceaggacata ceceagggaa cagtaacaaa tggaagcact taca
                                                                        354
<210> 737
<211> 198
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(198)
<223> n = A, T, C \text{ or } G
<400> 737
ctgccgctgc acacgctcgt tcttctctgc ctcagtgatg cgcttctcct cattgcggnc
                                                                         60
atceeggatg cecteactag acageteege getgtageee gtgggetetg egeceteate
                                                                        120
ctgcaagctc tcctggacat ggtagctcac cggctcgtac acggggggtg gtggggggg
                                                                        180
gggngctgtc atcaccag
                                                                        198
<210> 738
<211> 228
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (228)
<223> n = A, T, C \text{ or } G
<400> 738
gtgccatggc acacagectg ggtgcacacc cagegneete tettgcaggt gcaggtattg
                                                                         60
cagtccacct tgatcttggc gccggaagaa tanaggtcgt tgttatggac gcaagggcat
                                                                        120
teetteteea ceaegeagee acceeggeeg teatceatea geeegteggg geaeaeaeag
                                                                        180
ccactgacac actctgtgtg gnaatagccg gcggccagcg nctggcag
                                                                        228
<210> 739
<211> 378
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(378)
<223> n = A, T, C or G
<400> 739
aaaaaataca ggagtcgata gcagcagttg gtgacgagat ggcactcaga aacggcgttg
                                                                         60 <sup>°</sup>
acgtaattta ggacgtggaa tcataagcga aacagcacac tgtttgaata aagagcgagt
                                                                        120
cggnatttat atttgntttt cttttgtcat gattatttga tttttaagnt gctccagcta
                                                                        180
```

```
aggcattttt ttgtattagn atttctatta gggaaccttt cttattaggn ggnttgtatt
                                                                       240
                                                                       300 .
gtctggnttc taacatgcag gtagctgttt ggcagttaaa cacgtttaga gtaatttgag
ttacaacgtg tgaaactgag caaaaaagca gngataagnt tgggttacca taccaaatat
                                                                       360.
ttgttttccc actggaaa
                                                                       378
<210> 740
<211> 200
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (200)
<223> n = A, T, C or G
<400> 740
ccacttgagt ggntcctggc tgcttctgtg attgttaggt cttgagagat tatggacccg
                                                                        60
aggeattetg ggtaceceat caattggetg atggnettet atttgggetg egettettet
                                                                       120
aaaaagggga gctcaaaggt cttttttcc cccactgcag agctaaaaaa gtccctgtac
                                                                       180
gccatcttct cccagtttgg
                                                                       200
<210> 741
<211> 273
<212> DNA
<213> Homo sapien
<400> 741
ctgcttggca tcgtaatggg ccggtggcat catgagcccc agaatcagcc ttgccaggtc
                                                                         60
tecagagate teagacttea ggteagteat taagteeegg eeaaagtgag acttgaaggt
                                                                       120
ctgccggatc tgctgccgct ggacattgct gcggtgcgtg atgatatcga tgattgtgtc
                                                                       180
ttegteagte eegagteest teatggettt eegeageget ttggeatetg egteagggtt
                                                                       240
gaagtcattg gctgggcgca caggtccctt cag
                                                                       273
<210> 742
<211> 297
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(297)
<223> n = A, T, C or G
ctgcagttgc tccctttagg gttataaaat aatgacccaa atgttacatg tgttgatatt
                                                                        60
ataacttgtc agttactgat gtctgtggna tcctaccctc atctctgaaa gggataatac
                                                                       120
tgaataatta ttagaaaact ataaaacttc acactttgta ccattaaaac ctaaaatttt
                                                                       180
aatcttgncc ttttttacta tggatcagtc ggcactcggg aacagcagca aggaaaagag
                                                                       240
gcaaatttca ttcacatgtt ctgngntcat acctettctc tacctaattg ttcattt
                                                                       297
<210> 743
<211> 381
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(381)
```

```
<223> n = A,T,C or G
<400> 743
ctgcacctcc acctccttga agttgaagat actattgcca tcaaagccag cagccagctc
                                                                        60
tggacagtat gcctgcaggg aacctccatg ccggctcagt gacacactct ctgcagccag
                                                                       120
ggtaatgaac ttgtcctcag ctacaaaagc tgtgagcttg gctgtgctca cctccagggt
                                                                       180
taggtttagc agccgctttg ggggtaatgg ctcaggggca cggccttcta gctcagaagn
                                                                       240
agntectgaa gnetetagtg caagggatgg tacagtetea ggaaacacag nggetettag
                                                                       300
taggnetegg cactgtagag nggnggnate cecagagetg gngatgattt ggttgteate
                                                                       360
                                                                       381
caggaagcgg caacacgaca g
<210> 744
<211> 167
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(167)
<223> n = A, T, C or G
<400> 744
cagegngggg cteggagagg tgcteggatt ctegtagetg tgcegggaet taaccaccac
                                                                        60
catgtcgagc aaaagaanaa agaccaagac caagaagcgc cctcagcgtg caacatccaa
                                                                       120
tgtgtttgct atgtttgacc agtcacagat tcaggagttc aaagagg
                                                                       167
<210> 745
<211> 96
<212> DNA
<213> Homo sapien
<400> 745
ccacaaactc ctctggctgt actccctcct gcaggagacc ggcctcactg cactcagcag
                                                                        60
gctcttctcc ctgcgattca cttctgggac agtcac
                                                                        96
<210> 746
<211> 391
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(391)
<223> n = A, T, C or G
<400> 746
ccattacgca gccgcttcag caaacagggc tcctcccggc ccgagggcgg gaccacagtg
                                                                        60
gccgtcagca ggctgagatc cgtctctgag atgttgatgg ggatgtcggc agcagagccg
                                                                       120
acctttaggt gggacatacg catggagtcg tcacctgtga cccgggcagt gaaggggctg
                                                                       180
cctgggacgt gctgttcatt gtacttgact agaatgctgt agtcccccgg cagcacaggc
                                                                       240
aagtaggaca cgctgcnatg tcccatcctg gttgtcagtg cagtgttgct tgttcagtat
                                                                       300
ctcaagccca gaaagatgaa ttaatccttg aaggaaatga cattgagctt gtttcaaatt
                                                                       360
cageggettt gatteageaa gecacaacag t
                                                                       391
<210> 747
<211> 408
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc feature
<222> (1)...(408)
<223> n = A, T, C or G
<400> 747
aaagttgttt gtgccttttt atttttgttt ttaatgcttt gatatttcaa tgttagcctc
                                                                        60
aatttctgaa naccataggt agaatgtaaa gcttgtctga tcgttcaaag catgaaatgg
                                                                       120
atacttatat ggaaattctg ctcagataga atgacagtcc gtcaaaacag attgcttgca
                                                                       180
aaggggaggc atcagtgtcc ttggcaggct gatttctagg taggaaatgt ggnagcctca
                                                                       240
cttttaatga acaaatggcc tttattaaaa actgagtgac tctatatagc tgatcagttt
                                                                       300
tttcacctgg aagcatttgt ttctactttg atatgactgt ttttcggaca gtttatttgt
                                                                       360
tgagagngtg accaaaagtt acatgtttgc acctttctag gtgaaaat
                                                                       408
<210> 748
<211> 337
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(337)
<223> n = A, T, C or G
<400> 748
ggcggagaga ggcgagcacc gggaagggga gcgnggggcc gctggaatgg gtgaatttaa
                                                                        60
ggnccatcga gtacgtttct ttaattatgt tccatcagga atccgctgtg tggcttacaa
                                                                       120
taaccagtca aacagattgg ctgtttcacg aacagatggc actgtggaaa tttataactt
                                                                       180
gtcagcaaac tactttcagg agaaattttt cccaggtcat gagnctcggg ctacagaagc
                                                                       240
tttgtgctgg gcagaaggac agcgactctt tagtgctggg ctcaatggcg agattatgga
                                                                       300
gnatgattta caggcgttaa acatcaagta tgctatg
                                                                       337
<210> 749
<211> 261
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G
ccgggaggct ctgattattt acccaccaca ggtaggttgt gttctgaatc tcaggttcac
                                                                        60
aggttaaggc tacagcatcc tcatcctcca cggggttgga gttgttgctg gngatgaagg
                                                                       120
gtttgggtgg ctctgcatag actgtgatcg ncgtgactgt ggncctattg aggccagtgt
                                                                       180
ctgagttatg ggcttggcac gtataggatc cactattatt cacagngatg ttggggataa
                                                                       240
agagetettg ggnggattge t
                                                                       261
<210> 750
<211> 150
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (150)
```

```
<223> n = A, T, C or G
<400> 750
aacgctgang acatgacatc caaagattac tactttgact cctacgcaca ctttgnnatc
                                                                        60
cacgaggaga tgctgaagga cgaggtgcgc accetcactt accgcaactc catgtttcat
                                                                       120
aaccggcacc tcttcaagga caaggngnng
                                                                       150
<210> 751
<211> 288
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(288)
<223> n = A, T, C or G
aaaacttttg ttaagaaaaa ctgccagttt gtgcttttga aatgtctgtt ttgacatcat
                                                                        60
agtctagtaa aattttgaca gtgcatatgt actgttacta aaagctttat atgaaattat
                                                                       120
taatgtgaag nttttcattt ataattcaag gaaggatttc ctgaaaacat ttcaagggat
                                                                       180
ttatgtctac atatttgtgt gtgtgtgtgt gtatatatat gtaatatgca tacacagatg
                                                                       240
catatgtgta tatataatga aatttatgtt gctggnattt tgcatttt
<210> 752
<211> 248
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(248)
<223> n = A, T, C or G
<400> 752
ctggcactga ggattatatc catataagaa ttcaacagag aaacggcagg aagaccctta
                                                                        60
ctactgtcca agggatcgct gatgattacg ataaaaagaa actagtgaag gcgtttaaga
                                                                       120
aaaaqtttgc ctgcaatggt actgtaattg agcatccgga atatggagaa gtaattcagc
                                                                       180
tacagggnga ccaacgcaag aacatatgcc agttcctcgt agagattgga ctggctaagg
                                                                       240
acqatcaq
                                                                       248
<210> 753
<211> 346
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(346)
<223> n = A, T, C or G
<400> 753
ctgctagaaa acagggaaga tattagccaa tatggaattg ccaggttctt cactgaatat
                                                                        60
tttaacagtg tatgccaggg aacacacatt ctctttcgag aattcagctt cgtccaagcc
                                                                       120
acccccaca atagggnatc attttacgg gccttctgga gatgcttccg aactgtgggc
                                                                       180
aaaaatggcg atttgctgac catgaaagaa tatcactgtt tgctgcaatt actgtgtcct
                                                                       240
gatttcccgc tggagctcac tcagaaagca gccaggattg tgctcatgga cgatgccatg
                                                                       300
gactgcttga tgnctttttc agatttcctc tttgccttcc agatcc
                                                                       346
```

```
<210> 754
<211> 100
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (100)
<223> n = A, T, C or G
<400> 754
gtgccacagg cagccctggg anataggaag ctgggagcaa ggaaagggtc ttagtcactg
                                                                         60
cctcccgaag ntgcttgaaa gcactcggag aattgtgcag
                                                                        100
<210> 755
<211> 405
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (405)
<223> n = A, T, C or G
<400> 755
tgtgggccca cttcccaaat ctctggagga tctgcagctt actcataaca agatcacaaa
                                                                         60
gctgggctct tttgaaggat tggtaaacct gaccttcatc catctccagc acaatcggct
                                                                        120
gaaagaggat getgtttcag etgettttaa aggtettaaa teactegaat acettgaett
                                                                        180
gagetteaat cagatageea gactgeette tggneteeet gtetetette taacteteta
                                                                        240
cttagacaac aataagatca gcaacatccc tgatgagtat ttcaagcgtt ttaatgcatt
                                                                        300
gcagnatctg cgtttatctc acaacgaact ggctgatagt ggaatacctg gaaattcttt
                                                                        360
caatgngnca tccctggntg agctggatct gtcctataac aagct
                                                                        405
<210> 756
<211> 306
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (306)
<223> n = A, T, C or G
<400> 756
ccttgggaaa ttacctggaa atgcgactga aatcttcctt cctgaggggt ctgggctctt
                                                                         60
ggaaatcaaa ccctctcagg ttgggtggct ggacgattct cctcacactt anaatgggac
                                                                        120
aaggggaacc aggaggccc caaggggatc cctgggntcc acacgaactc ctcctaccct
                                                                        180
cattgngtga cagcagccat gcctcctcct ggggatcagg atctattacc tgtgcctgga
                                                                        240
gaggagggga ctcctcttct cacccgctgg nctctggaca catactgtcc aattcccctg
                                                                        300
tggcag
                                                                        306
<210> 757
<211> 321
<212> DNA
<213> Homo sapien
<220>
```

```
<221> misc feature
<222> (1)...(321)
<223> n = A, T, C or G
<400> 757
ctggagggag: gntccctggg aggtttttgt ggattccttc tgcagngact cccctggttt
                                                                        60
ctggntctgg ggacccagng tccaggcgca gncttttagc acttctcagt gtagacgttg
                                                                       120
acagggntct tttcccgctt gaatcctgct gagtccccaa atctcttgac ttgtcttggn
                                                                       180
tacagncacc accagagetg etencagntt tgacaaaage agttgetget gaagngateg
                                                                        240
ttttgaatcc tatcatagca ctggcaggtc ccggnaaatt cttacagtca gcaggcggac
                                                                        300
ctcgtgtgag ttgaatattc c
                                                                        321
<210> 758
<211> 278
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G
<400> 758
cgctcggcaa gntctcccag gagaaagcca tgttcagttc gagcgccaag atcntgaagc
                                                                         60
ccaatggcga gaagccggac gagttcgagt ccggcatctc ccaggctctt ntggagctgg
                                                                        120
agatgaactc ggacctcaag gctcagctna gggagctgaa tattacggca gctaaggaaa
                                                                        180
ttgaagttgg tggtggtcgg aaagctatca taatctttgn tcccgntcct caaacctgcc
                                                                        240
cgggcggccg cttcgagccc tatagtgagg cgnattag
                                                                        278
<210> 759
<211> 401
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A, T, C or G
<400> 759
qcaaactqca aaccatqqtq aqaaattqac qacttcacac tatqqacaqc ttttcccaaq
                                                                         60
atgtcaaaac aagacteete ateatgataa ggetettace eeettttaat ttgteettge
                                                                        120
ttatgcctgc ctctttcgct tggcaggatg atgctgtcat tagtatttca caagaagtag
                                                                        180
cttcagaggg taacttaaca gagtatcaga tctatcttgt caatcccaac gttttacata
                                                                        240
                                                                        300
aaataagaga teetttagtg cacecagnga etgacattag cageatettt aacacageeg
ngtgttcaaa tgtacagngg nccttttcag agntggactt ctagactcac ctgttctcac
                                                                        360
tccctgnttt aattcaaccc agccatgcaa tgccaaataa t
                                                                        401
<210> 760
<211> 346
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (346)
<223> n = A,T,C or G
```

```
<400> 760
ccgaggtttg gatcatggga gaacagcaga aaggggttat tgagggaacc tacactgttc
                                                                        60
tagetgeace ceatgeeett eteagaggaa ageetggeat tgattagata etgggeeaga
                                                                       120
ctaatactgg cagcagagec agtgatagta acctgectae cagaggagee ttecactggg
                                                                       180
ttggcaattt tgatctgggc cccggacatc tggcggatct cattaatgtt ggcgccttgg
                                                                       240
cgcccgatta tgcagccaat taagttattt ggaatggnga gttcatgggt ggtttgagta
                                                                       300
gatgcatcca aacttgccca atagcctttc acctntggag agacct
                                                                       346
<210> 761
<211> 256
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(256)
<223> n = A, T, C or G
<400> 761
gagacagact gggtgatgac gctgaatctg cagaggtgct ggtgaccaat tcccctaaag
                                                                        60
catctacttg tctcctcaaa ctgtgtaaag tgccctctgt ctgccgcttt cctttaatta
                                                                       120
atacttctgc ttgcttggac atacagtgtc ggagttggnc ctgaaaagtg tgataagact
                                                                       180
taggntttta cacagnaaga aatgtaccag aactgctgct cagcttcctc acatacattt
                                                                       240
gataggcaaa tctagc
                                                                       256
<210> 762
<211> 321
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(321)
<223> n = A, T, C or G
<400> 762
tggactctgg antgatgctg gaagtagata cgaaaatgng aagaacaatg gaacagcaca
                                                                        60
ctttctggag catatggctt tcaagggcac caagaagaga tcccagttag atctggaact
                                                                       120
tgagattgaa aatatgggtg ctcatctcaa tgcctatacc tncagagagc agactgtata
                                                                       180
ctatgccaaa gcattctcta aagacttgcc aagagctgta gaaattcttg ctgatataat
                                                                       240
acaaaacagc acattgggag aagcagagat tgaacgtgag cgtggagtaa tccttagaga
                                                                       300
gatgcaggaa gttgaaacca a
                                                                       321
<210> 763
<211> 348
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(348)
<223> n = A, T, C or G
<400> 763
tgagaaaaca taaagtaacc agcagatttc aatattaaaa agaagtggtt cntcctaaaa
                                                                        60
aaggtnttag atcatagagt tgggattagg gtaggggata cctattaatc tggnctggaa
                                                                       120
aaaaagngtg tggagaaggg gagntgtatt gntttctcac aagaggcaaa cttcagncaa
                                                                       180
acaatgaaga gatagtaggn agggagatgt gtgntagacc aaagactttc tgattgctga
                                                                       240
```

```
taataacaaa tttagcagct ntctacaagt caattaaaat accattctct gagacatttt
                                                                        300
cagagaggag ctaactaaca cccacccagg nggaaaaatc attctaca
                                                                        348
<210> 764
<211> 374
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(374)
<223> n = A, T, C or G
<400> 764
agenaagaag gaageteetg eeecteetaa agetgaagee aaagegaagg etttaaagne
                                                                         60
caagaaggca gcgttgaaag gtgtccacag ccacaaaaag aagaagatcc ncacgtcacc
                                                                        120
caccttceng engecgaaga cactgegact eeggaqacaq eecaaatate eteggaagaq
                                                                        180
cgctcccagg agaaacangc ttgnccacta tgctatcatc aagtttccgc tgaccactga
                                                                        240
gnctgccatg aagaagatag aagacaacaa cacacttgtg ttcattgngg atgttaaagc
                                                                        300
caacaagcac cagattaaac aggctgngaa gaagctgtat gacattgatg tggccaaggt
                                                                        360
caacaccctg attc
                                                                        374
<210> 765
<211> 288
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
 <222> (1)...(288)
<223> n = A, T, C or G
<400> 765
aaatacaata attotgttat tgataaaatt taaqqcattt toattqcctt ttqcaqattt
                                                                         60
actcataact acctaacaag gaaagaaggt ataattattt cagattggat tatttattct
                                                                        120
aaaattaaat tottoactaa tttattotaa gatgaattta atagtocato aggaaattgg
                                                                        180
nttttataaa gcttatttta tgggcataaa atacaggaaa aggtaataat aaatgccaaa
                                                                        240
ccgtctcttt actttatgaa gccaaatatt tcctcagact tggttttt
                                                                        288
<210> 766
<211> 424
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A, T, C or G
<400> 766
ttgtggttgt gcctgagggc tctgcttccq acactcatga acaggctatc ttgcggttgc
                                                                         60
aagtcaccaa tgttctgtct cagcctctga ctcaqgccac tgttaaacta qaacatgcta
                                                                        120
aatctgttgc ttccagagcc actgtcctcc agaaqacatc cttcacccct gtaggggatq
                                                                        180
tttttgaact aaatttcatg aacgtcaaat tttccagtgq ttattatgac ttccttgtcq
                                                                        240
aaqttqaaqq tqacaaccqq tatattqcaa ataccqtaqa qctcaqaqtc aaqatctcca
                                                                        300
ctgaagttgg catcacaaat gttgatcttt ccaccgngga taaggatcag agcattgcac
                                                                        360
ccaaaactac ccgggtgaca tacgcagcca aagccaaggg cacattcatc gcagacagcc
                                                                        420
acca
                                                                        424
```

```
<210> 767
<211> 302
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(302)
<223> n = A, T, C or G
<400> 767
ggetttetca ataageetca getttetaag atetaacaag atageeaceg agateettat
                                                                         60
cgaaactcat tttaggcaaa tatgagtttt attgtccgtt tacttgtttc agagtttgta
                                                                        120
ttgtgattat caattaccac accatctccc atgaagaaag ggaacggtga agtactaagc
                                                                        180
gctagaggaa gcagccaaqt cqnttagtqq aagcatqatt ggtqcccaqt tagcctctqc
                                                                        240
aggatgtgga aacctccttc caggggaggt tcagtgaatt gtgtaggaga ggttgtctgt
                                                                        300
gg
                                                                        302
<210> 768
<211> 94
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(94)
<223> n = A, T, C or G
<400> 768
ctgatctaaa agaagttact gaggaagatt tgaataatca ctttaagtct ttgggaagca
                                                                         60
gnnatttgaa atnttgaggt gacagncttt taag
                                                                         94
<210> 769
<211> 69
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1) ... (69)
<223> n = A,T,C or G
<400> 769
ctgcaagacg actccaaccc aacaacaacc. agatgngctn cagcccagcc ggncttcagt
                                                                         60
tccatattt
                                                                         69
<210> 770
<211> 222
<212> DNA
<213> Homo sapien
<400> 770
ctgaacgcaa accagccact ttaattaagc taagccctta ctagaccaat gggacttaaa
                                                                         60
cccacaaaca cttagttaac agctaagcac cctaatcaac tggcttcaat ctacttctcc
                                                                        120
cgccgccggg aaaaaaggcg ggagaagccc cggcaggttt gaagctgctt cttcgaattt
                                                                        180
gcaattcaat atgaaaatca cctcggagct ggtaaaaaga gg
                                                                        222
```

tagaataata tttt

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tctagttaat tcattatgca gaaggtatag gggttagncc ttgctatatt atgcttggnt
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gcctatactt tatttgggta aatgg
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cagttagttc attaaagttt tggaaattct cagacagtgc agtggtatca gaaacttgta
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tgccagactg gagtgcagtg gtgcgatctg ggctcactgc aatctccacc tcccgggttc
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agettgacca atgactggga agatcacttg gcagngaagc atttttc
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ccgcctttga gctggtcttc atagtcctgg ctgagcacta caaggtggtg gtaaatggaa
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atcacacgtt ccacc
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                                                                       180
gcgcgcacgg ggcgccatag gcttcggggt ccaagcgcgt gtcgttttgg gggagcagcg
ccgcctctgc ggcccagagt tgcgccatca gcagcggcag cagcttcgcc agagcccggg
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                                                                       300
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cgataggaag gagggagggg acccagacgt gcctntgccc tgcctgtggt ctgccgcgtc
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tetecatect gecatggegt cetggeetgt gaggacatgg ggegeetggg agegggggg
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gaggetggge ageaetggge cagaggegte etggteaetg etceaeetgg teaetgetee
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ggggtcccgg gatggtggag ggggccgggg tcggggcctg caggatggtc atggtcgggt
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                                                                       300
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aggcactacc agcaacgtca ggaagtgctc agccattgtg gtgtacacca aggcgaccac
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gccggctgcg atgaggaagt agcccacgtt gacaaactgc atggcactgg acgacagtgg
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tgtgtcnntg cagcgacgag gatggcactg gatggcttag agaaactagc accacaacct
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cnnggtgtgc ttgtcaaaga gatattccgc cnagccanat tcgggcgctc ccatcttgcg
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tcacgtcctc attgatcagc ggcggtgcct cggaggaggc gctgcccggc gccggggccc
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tecceagggg etgecagage cetgtgtgee ttgeegeatt eccetgatge agettttgge
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aactgaaagg cagggctctc gctgagtgca cctggggctt cctgagccca tctgcggcgg
                                                                       240
ecceacetg geetaggtge tgagtgeage tgetgeagae agececteec teettagtgg
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cagaaqcagg gctgggggag ggqtggagcc attcagcctc aggcaccctc acagctaggt
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58
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<213> Homo sapien
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aggatgagtt tggageggta ctccttcagc cgctgcacgt tggtctgcag ggactccgtg
                                                                    180
gacttgttcc gcctcctcgg atccacagaa atgccgatgg tccgggccac cttcttgtga
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atgccggcca ccctgagctc ctccaggctg aagccgcggc cggcgcgcac cttcgtgtgg
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taccgaaccg tggggcagcg cacgatgggc cggatgggac ccgacgcggg gcgcggggcg
                                                                    360
atgcggcgcg cettggcttg ccgggcctta cgtctgcgga tcttacgggc cggctggttg
                                                                    420
aaccacgtgg ccacgcgccg ctgccagtcc ttgtggaagt ggggcttcaa gaccatgcca
                                                                    480
ttccggctgg gcgccatggc tgcctacggc cctgcggctc ctggtcgacg cggccqcgaa
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. 254

tt							542
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<210> 908 <211> 238 <212> DNA <213> Homo sapien					

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ggaagttgtc cggaagcacg gtcggagggg tcgacacgtc cctctcggac ttggcggggg
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tgccacggct gcgacggctc acacggcttg cgggcctgct gaantanaag ccgcggtccc
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cacagacgaa ctggagggtg tccaccagct ccccgncgca cagggtctca ctggggcggn
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aagcagcaat gcancacgag gcgaaggcca anaaggngan aagcaccanc atcgacttcc
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ccattgggat tcccattggt gtctgga
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<211> 574
<212> DNA
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tagcacagta cgtctccagg agggccaggt cacagctgcg gaaacagcac tcctcaacga
                                                                       240
tgccacggct gcgacggctc acacggcttg cgggcctgct gaagtagaag ccgcggtccc
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cacagacgaa ctggagggtg tccaccagct ccccgccgca cagggtctca ctggggcggt
                                                                       360
aagcagcaat gcagcacgag gcgaaggcca agaaggtgag aagcaccagc atcgacttcc
                                                                       420
ccattgggat tcccattggt gtctggaagc cggcgacgct gccgcccacc tccctgctgc
                                                                       480
gtgtcgcaaa ccgaacagcg ggcgttggcc ctcctgccgg acactcctct gccagcgccg
                                                                       540
ctctggccga gtcgcggggg ccgaatgtgc qacg
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<211> 139
<212> DNA
<213> Homo sapien
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                                                                        60
gccccccggg ccgtcttccc ctccatcgtg gggcgcccca ggcaccaggg cgtgatggtg
                                                                       120
ggcatgggtc agaaggatt
                                                                       139
<210> 920
<211> 576
<212> DNA
<213> Homo sapien
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<221> misc_feature
<222> (1)...(576)
<223> n = A, T, C or G
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<210> 924 <211> 216 <212> DNA <213> Homo sapien					
<400> 924					

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cggggtcccg ggatggtgga gggggccggg gtcggggcct gcaggatggt catggtcggg
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tggcagctgc gagagtgaca catggtgagc cgagcg
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                                                                       120
cattggctgt gttggtgacg ttgtcattgc aacagaatgg gggaaaggca ctgttctctt
                                                                       180
tgaagtaggg tgagtcctca aaatccgtat agttggtgaa gccacagcac ttgagccctt
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tcatggtggt gttccacact tgagtgaagt cttcctggga accataatct ttcttgatgg
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caggcactac cagcaacgtc aggaagtgct cagccattgt ggtgtacacc aaggcgacca
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cagcagctgc aacctcagca atgaagatga ggaggaggat gaagaagaac gtcacgaggg
                                                                       420
cacacttgct ctcagtctta ncaccatagc agcccaggaa accaagagca aagaccacaa
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cgccggctgc gatgaggaag tagcccacgn tgacaaactg catggcactg gacgacagtg
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gcccgaagat cttcagaaag gatgccccat cgattgacac ccagatgccc actgccaaca
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gccagaaggt tgggcggcag gaactgggtc atcttgccaa gtcgcgtagc gccctcctcg
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tgcttcggct tccactccgg gggcgtccac gtccgtctga ttccgtcgcc cgctaagcga
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gaagcccaga gagaggtagg tgtaggaggc ctgcaggtac aaattgacca ggctgttgac
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gatggtcccg gaggttgcaa gcggagagga aatcggaggg cggtcggagg ctggaagaga
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tccgccctca cttggggggc caaaaagggt	gaaaacactg agccccacaa ttgggccagg	catggagaag ggggcgccgg aagaaaactt tgaatgcaaa tcgcggcaca	gcgggagacc gaggtggagt tcttgtcacc	ctacagtaaa tttccggtca aaactacaca	acaaacgaca cccaaagaga caaatcgacc	240 300 360 420 480
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<210> 942

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<210> 943 <211> 130 <212> DNA <213> Homo sapien					
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attccaaggg cctgtttaca tggcagcana atccatc	637
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<210> 948 <211> 575 <212> DNA <213> Homo sapien	
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266

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<211> 693
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (693)
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cattggctgt gttggtgacg ttgtcattgc aacagaatgg gggaaaggca ctgttctctt
                                                                       180
tgaagtaggg tgagtcctca aaatccgtat agttggtgaa gccacagcac ttgagccctt
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tcatggtggt gttccacact tgagtgaagt cttcctggga accataatct ttcttgatgg
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caggcactac cagcaacgtc aggaagtgct cagccattgt ggtgtacacc aaggcgacca
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cagcagctgc aacctcagca atgaagatga ggaggaggat gaagaagaac gtcacgaggg
                                                                       420
cacacttgct ctcagtctta gcaccatagc agcccaggaa accaagagca aagaccacaa
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cgccggctgc gatgaggaag tagcccacgt tgacaaactg catggcactg gacgacagtg
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gcccgaagat cttcanaaag gatgccccat cgattgacac ccagatgccc actgccaaca
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gggctgcacc acacagaaag atgagcaaat tgaagaggat catcatggtc ttaatgaagc
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tgaagcactg catggnggct cctgttcagg gct
                                                                       693
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<211> 607
<212> DNA
<213> Homo sapien
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cocqtqctct qcqtqacqca qtccatccac agcccttqt acatqqcctq qqccqtqatq
                                                                       120
atgttgtcac ccgcatagga gctcatctgc cactgcggga tggcggtgca ggccaccaga
                                                                       180
cccacccagc ccagcagggc catggagaag cccagcaact gcaggcccga attggccatt
                                                                       240
tecgecetea gaaaacaetg ggggegeegg gegggagaee etacagtaaa acaaaegaea
                                                                       300
cttggggggc agcccacaa aagaaaactt gaggtggagt tttccggtca cccaaagaga
                                                                       360
caaaaagggt ttgggccagg tgaatgcaaa tcttgtcacc aaactacaca caaatcgacc
                                                                       420
cctccagtga agcgatggcc tcgcggcaca gggagtagga tacgccggga gggtggttcc
                                                                       480
agacaaaatt ggtggtcccc gaaggccagg cggttccctc cgggcgctct cggcgaccct
                                                                       540
aggcaaacaa aaggtggagg ggccgtctgg gcgcgtttct gagcgccggc aagtcccaaa
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gtatcct
                                                                       607
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<211> 372
<212> DNA
<213> Homo sapien
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tettetttgt cagecetttt teettggage cagtgteeae gaagaagagt tttteatttg
                                                                       120
gggcetetga caacaageca eegetegtge geteetgtag eegeacgtet tecaggaact
                                                                       180
ggtcaacctc cagccccagc ggctcctgag caagccgccg ccagccccgc ttcttatttc
                                                                       240
ttgggcctcg ccgccgccgc ctcagcgctg ggtccaccga agtgggccgc agccccagga
                                                                       300
aaccagaatc ggcatcgctt ttcgagctgc gcttcccacc aacgccactg cctgtcgacg
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cggccgcgaa tt
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<210> 955 <211> 189 <212> DNA <213> Homo sapien	
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<210> 956 <211> 216 <212> DNA <213> Homo sapien	
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<210> 961 <211> 490 <212> DNA <213> Homo sapien					
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<210> 962 <211> 159 <212> DNA <213> Homo sapien					
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gcgatggcgg cgcgcgggcn gnggacagan agaagccggt gtaagctcgc gggttgctcc
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ggagcgggcg ggggccggac gtcgacgcgg ccgcgaatt
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<211> 217
<212> DNA
<213> Homo sapien
<220>
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<222> (1)...(217)
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ggggccgctg cgggctccnn gagagggtcg aaggtgaaga tctcaggacc ggagccccgc
                                                                       120
cggggtcccg ggatggtgga gggggccggg gtcggggcct gcaggatggt catggtcggg
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tggcagctgc gagagtgaca catggtgagc cgagcgt
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<212> DNA
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                                                                       120
atgttgtcac ccgcatagga gctcatctgc cactgcggga tggcggtgca ggccaccaga
                                                                       180
cccacccage ccagcaggge catggagaag cccagcaact gcaggecega attggecatt
                                                                       240
                                                                       300
tecgecetea gaaaacaetg ggggegeegg gegggagaee etacagtaaa acaaacgaea
cttggggggc agccccacaa aagaaaactt gaggtggagt tttccggtca cccaaagaga
                                                                       360
caaaaagggt ttgggccagg tgaatgcaaa tcttgtcacc aaactacaca caaatcgacc
                                                                       420
cctccagtga agcgatggcc tcgcggcaca gggagtagga tacgccggga gggtggttcc
                                                                       480
aganaaaatt ggtggtcccc gaaggccagg cggttccctc cgggcgctct cggcgaccct
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<210> 965
<211> 321
<212> DNA
<213> Homo sapien
<220>
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<223> n = A,T,C or G
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acaccegege agtggaacga egegegeacg gggegecata geegeetetg eggeecagag gegecagagg eggeggagag cegatangaa ggagggaggg	ggcttcgggg ttgcgccatc gtggaggtgc	tccaagcgcg agcagcggca	tgtcgttttg gcagcttcgc	ggggagcagc cagagcccgg	120 180 240 300 321
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gagtggagag tactggattg					180
ctgcaacatg gagactggtg					240 300
gaactggtac atcagcaaga gaccgatgga ttccagttcg					360
ccagctgacc ttcctgcgcc	tgatgtccac	cgaggcctcc	cagaacatca	cctaccactg	420
caagaacage gtggcctaca					480 540
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aaccaccaag acctcccgcc					642
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_					
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gaactggtac atcagcaaga gaccgatgga ttccagttcg					300 360
ccagctgacc ttcctgcgcc	tgatgtccac	cgaggcctcc	cagaacatca	cctaccactq	420
caagaacagc gtggcctaca	tggaccagca	gactggcaac	ctcaagaagg	ccctgctcct	480
ccagggctcc aacgagatcg cactgtcgat ggctgcacga					540 600
aaaccaccaa gaccttccgc	ctgcccatca	tcgatgtggc	ccccttggac	uccyaacaca	650
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cagccgcaag aaccccgccc gcacctgccg tgacctcaag atgtgccact ctgactggaa
gagtggagag tactggattg accccaacca aggctgcaac ctggatgcca tcaaagtctt
                                                                       180
ctgcaacatg gagactggtg agacctgcgt gtaccccact cagcccagtg tggcccagaa ·
                                                                       240
                                                                       300
gaactggtac atcagcaaga accccaagga caagaggcat gtctggttcg gcgagagcat
gaccgatgga ttccagttcg agtatggcgg ccagggctcc gaccctgccg atgtggccat
                                                                       360
ccagctgacc ttcctgcgcc tgatgtccac cgaggcctcc cagaacatca cctaccactg
                                                                       420
caagaacagc gtggcctaca tggaccagca gactggcaac ctcaagaagg ccctgctcct
                                                                       480
ccagggctcc aacgagatcg agatccgcgc cgagggcaac agccgcttca cctacagcgt
                                                                       540
                                                                       600
cactgtcgat ggctgcacga gtcacaccgg nagcctgggg caagacagtg attgaataca
aaaccaccaa gacctcccgc ctgcccatc
                                                                       629
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<211> 222
<212> DNA
<213> Homo sapien
<400> 969
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gegettggtt cttggggtte tecaggatte cageetegta getgatgtge atgaggttet
                                                                       120
catccatgct ccacgggttc ttgggagtga ccgggatggg aatcccgtgt tgctttgcgt
                                                                       180
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<212> DNA
<213> Homo sapien
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acggacggga agcaacgga
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<211> 111
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ccccattcgt cagccccacg cctcctccag gatccgggcc cagctcgaat t
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<210> 972
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<212> DNA
<213> Homo sapien
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<221> misc_feature
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<223> n = A, T, C or G
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PCT/US00/35596

cagccgcaag aaccccgccc gagtggagag tactggattg ctgcaacatg gagactggtg gaactggtac atcagcaaga gaccgatggac ttcctgcgcc cagctgacc ttcctgcgcc caagaacagc gtggcctaca ccagggctcc aacgagatcg cactgtcgat ggctgcacga aaaccacca	accccaacca agacctgcgt accccaagga agtatggcgg tgatgtccac tggaccagca agatccgcgc	aggetgeaac gtaceceact caagaggeat ccagggetce cgaggeetce gactggeaac cgagggeaac	ctggatgcca cagcccagtg gtctggttcg gaccctgccg cagaacatca ctcaagaagg agccgcttca	tcaaagtctt tggcccagaa gcgagagcat atgtggccat cctaccactg ccctgctcct cctacagcgt	120 180 240 300 360 420 480 540 600
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<210> 974 <211> 180 <212> DNA <213> Homo sapien					
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<210> 976 <211> 59 <212> DNA <213> Homo sapien					
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<212> DNA
<213> Homo sapien
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cggttt
                                                                         66
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<211> 114
<212> DNA
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agaggtggac accttgtagg acttctgggt cacccgtcga cgcggccgcg aatt
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ggctgtgagc agtgttggtg gcatacctgt cacagcatct agcaaagcac ctgaatt
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<223> n = A, T, C or G
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ggaggcagge gggccgaacc aggcggagat cctagaagga gcggagaagg tcgacgcggc
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cgcgaatt
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<210> 981
<211> 184
<212> DNA
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<222> (1)...(184)
<223> n = A,T,C or G
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                                                                       180
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aatt
                                                                        184
<210> 982
<211> 98
<212> DNA
<213> Homo sapien
<400> 982
tecactagte cagtgtggtg gaattegegg eegegtegae egaaceetga accetaeggt
                                                                         60
cccgacccgc gggcgaggcc gggtacctgg gctgggat
                                                                         98
<210> 983
<211> 425
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G
<400> 983
                                                                         60
geoggatatg gteetgeegg tggeagecta tgggetgate etgatggeea tgetgtggeg
cggcctggcc cagggcggga gtgccggctg gggcgcgctg ctcttcacgc tctctgatgg
                                                                        120
egtgetggee tgggacacet tegeceagee eetgeeecat geceneetgg tgateatgae
                                                                        180
cacctactat gctgcccagc tcctcatcac actgtcagcc ctcaggagcc cggtgcccaa
                                                                        240
gactgactga ctagggaget tgaagggeeg gtgtteagge ceteteetee tgeaaggace
                                                                        300
tgggcctccc agcccagccc agcctgagaa ataccctcag cagcgaagct tcctgacgcc
                                                                        360
                                                                        420
tgtctgcagg cgccgctgcc gccgtcgctt ctggctgaag acgtttgagg acgatttgcg
                                                                        425
gaatt
<210> 984
<211> 148
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(148)
<223> n = A, T, C \text{ or } G
<400> 984
tectnageea gggagaeagg gaccaggeag cacaggeetg ceageaggag gatgeeceae
                                                                         60
                                                                        120
gagacagaag acggeattgt cgattcactg teccaggtca gtggtgggtc gacgcggccg
                                                                        148
cgaattccac cacactggac tagtggat
<210> 985
<211> 461
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(461)
<223> n = A, T, C or G
<400> 985
ggtggacacc accctcaaga gcctgagcca gcagatcgag aacatccgga gcccagaggg
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cagccgcaag aaccccgccc gcacctgccg tgacctcaag atgtgccact ctgactggaa gagtggagag tactggattg accccaacca aggctgcaac ctggatgcca tcaaagtctt ctgcaacatg gagactggtg agacctgcgt gtaccccact cagcccagtg tggcccanaa gaactggtac atcancaaga accccaagga caagaggcat gtctggttcg gcgagagcat gaccgatgga ttccagttcg agtatggcgg ccagggctcc gaccctgccg atgtggccat ccagctgacc ttcctgcgcc tgatgtccac cgaggcctcc canaacatca cctaccactg caagaacagc gtggcctaca tggaccanca nactggcaac c	120 180 240 300 360 420 461
<210> 986 <211> 138 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(138) <223> n = A,T,C or G	
<400> 986 gagcggctgc tgaaggcccg ggggccagag gtggacacct tgtangactt ctgggtcacc ctgatggaca tggtagaggc aggagtggag gcaggcgggc cgaaccaggc ggagatccta gaaggagcgg aggtcgnc	60 120 138
<210> 987 <211> 555 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)(555) <223> n = A,T,C or G	
<pre><400> 987 geggcegccc ttttttttt tttttttag tggtataact atatttattg tgcctgagag gcaaggtgag ggaaaaatct caacagaagc aagtttgggg aaaatctgga gtccccagta aaaagcagga aggtetetge tgtactcate acagaatggg agagaggget etcaatagat cattccettt gtttetecec tgggettett gagetteteg aagttetea ggatgatgte atataacaca gcataagcat tgcggatete catgaccate ageeggatgt eccggtaete tgcetcatec agetegtga ccagetgeeg ataateacec acatgggget gettggetge tttagteact gcatcaccac gctcagagaa atacttagag atttgagtgt ggaagcette tanettggtg tggaggetgg tcatcagete aaacacette tectggacag ccactccaaa attgttacca tcetcaatec gaggtatetg cagetgeac caggtggtga ccaggttgag ctgetcaatg acate</pre>	60 120 180 240 300 360 420 480 540 555
<210> 988 <211> 318 <212> DNA <213> Homo sapien	
<400> 988 gacggcgcgg gcgacctacg aacagctttg aggaagcccc gacagtggcg gcgtccagtg cctccgaggg cggcgaccgc ggctccgcag cctcccag ccgctccgcc cggttccggg gagtcggtcg ggacaaaatg gcctcccctc cccctcagg gcttctcggc cgggacgctc ccacgggcga gcaagcctgc tctgccgtcg aggaggcgca gcgggcgtga ggacagtctc tctcccgagc ggaaactccc tgctagcacg cggcgagggc agcgaagaag gacccctaag tcgacgagct cagttaca	60 120 180 240 300

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<210> 989
<211> 177
<212> DNA
<213> Homo sapien
<400> 989
gacattttat gacctctccc aataggggca gaggtgagca cccctggtga aaagttaaga
                                                                        60
                                                                       120
ctcagtgagt ataaatacgc caagaagagc tgtggcttct ttcactggtg tcctcagaaa
ggctgtgagc agtgttggtg gcatacctgt cacagcatct agcaaagcac ctgaatt
                                                                       177
<210> 990
<211> 144
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1) ... (144)
<223> n = A, T, C or G
<400> 990
qtqaqcaccc ntqqtqaaaa qttaaqactc aqtqaqtata aatacqccaa qaaqaqctqt
                                                                        60
ggettettte actggtgtee teagaaagge tgtgageagt gttggtggea tacetgteae
                                                                       120
                                                                       144
agcatctagc aaagcacctg aatt
<210> 991
<211> 659
<212> DNA
<213> Homo sapien
<400> 991
ggtggacacc accetcaaga gcctgageca gcagatcgag aacatccgga gcccagaggg
                                                                        60
cagccgcaag aaccccgccc gcacctgccg tgacctcaag atgtgccact ctgactggaa
                                                                       120
gagtggagag tactggattg accccaacca aggctgcaac ctggatgcca tcaaagtctt
                                                                       180
etgcaacatg gagactggtg agacetgcgt gtaccccact cageccagtg tggcccagaa
                                                                       240
gaactggtac atcagcaaga accccaagga caagaggcat gtctggttcg gcgagagcat
                                                                       300
gaccgatgga ttccagttcg agtatggcgg ccagggctcc gaccctgccg atgtggccat
                                                                       360
ccagctgacc ttcctgcgcc tgatgtccac cgaggcctcc cagaacatca cctaccactg
                                                                       420
caagaacagc gtggcctaca tggaccagca gactggcaac ctcaagaagg ccctgctcct
                                                                       480
ccagggetee aacgagateg agateegege egagggeaac ageegettea cetacagegt
                                                                       540
cactgtcgat ggctgcacga gtcacaccgg agcctggggc aagacagtga ttgaatacaa
                                                                       600
                                                                       659
aaccaccaag acctcccgcc tgcccatcat cgatgtggcc cccttggacg ttggtgccc
<210> 992
<211> 226
<212> DNA
<213> Homo sapien
<400> 992
teegetgeae tgggtttgee ggattettgg getteecaea tactgettea catteaggaa
                                                                        60
gtttatetee aacageetta tttatecaet gettettate atttaaggtg tataeteeat
                                                                       120
ctccttctgt gcgcagtttg tagtagttct tacactggta gcgaaccgag tgctccacat
                                                                       180
agccatgtgc aatctcgggg ggcttcgggc agccgtcatc tgcgat
                                                                       226
<210> 993
<211> 160
<212> DNA
<213> Homo sapien
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<220>
<221> misc feature
<222> (1)...(160)
<223> n = A, T, C or G
<400> 993
ctcgtgtnng agcgnctgct gaaggcccgg gggccanagg nggacacctt gtacgacttc
                                                                        60
tgggtcaccc tgatggacat ggtanangct ggagtggagg caggcgggcc gaaccaggcg
                                                                       120
gagatectag aaggagegga ggtegaegeg geegegaatt
                                                                       160
<210> 994
<211> 622
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(622)
<223> n = A,T,C or G
<400> 994
nagectgane cageagateg agaacateeg gageceagag ggeageegea agaaceeege
                                                                        60
ccgcacctgc cgtgacctca agatgtgcca ctctgactgg aagagtggag agtactggat
                                                                       120
tgaccccaac caaggctgca acctggatgc catcaaagtc ttctgcaaca tggagactgg
                                                                       180
tgagacctgc gtgtacccca ctcagcccag tgtggcccag aagaactggt acatcagcaa
                                                                       240
gaaccccaag gacaagaggc atgtctggtt cggcgagagc atgaccgatg gattccagtt
                                                                       300
cgagtatggc ggccagggct ccgaccctgc cgatgtggcc atccagctga ccttcctgcg
                                                                       360
cctgatgtcc accgaggcct cccagaacat cacctaccac tgcaagaaca gcgtggccta
                                                                       420
catggaccag cagactggca acetcaagaa ggccctgctc ctccagggct ccaacgagat
                                                                       480
egagateege geegagggea acageegett cacetacage gteactgteg atggetgeae
                                                                       540
gagtcacacc ggagcctggg gcaagacagt gattgaatac aaaaccacca agacctcccg
                                                                       600
cctgcccatc atcgatgtgg cc
                                                                       622
<210> 995
<211> 158
<212> DNA
<213> Homo sapien
<400> 995
aataagattt tgccagaggg gaaggctcga ttgtgctgtt aataacttaa taatgacaaa
                                                                        60
ataatgaggt gtatatgctt tacatgcaat gttatatagt gaattgttct gattcttaat
                                                                       120
tgtaagtctg gtttttttat ctgtaagata attgtgtg
                                                                       158
<210> 996
<211> 295
<212> DNA
<213> Homo sapien
<400> 996
cggccgcgtc gactctcgga gcggagacgg caaatggcgg acttcgacac ctacgacgat
                                                                        60
cgggcctaca gcagcttcgg cggcggcaga gggtcccgcg gcagtgctgg tggccatggt
                                                                       120
tecegtagee agaaggagtt geceacagag ceceetaca cagcataegt aggaaateta
                                                                       180
cctttcaata cggttcaggg cgacatagat gctatcttta aggatctcag cataaggagt
                                                                       240
gtacggctag tcagagacaa agacacagat aaatttaaag gattctgcta tgtag
                                                                       295
<210> 997
<211> 125
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<212> DNA
<213> Homo sapien
<400> 997
cggccgccct ttttttttt ttttttaagg ttttttggct gtaagtttat tcaatgcaaa
                                                                        60
agaatcctct ccaattttac tgaggtggct gaccacgtcc acgaccaaat ccgcctctaa
                                                                       120
actgg
                                                                       125
<210> 998
<211> 152
<212> DNA
<213> Homo sapien
<400> 998
gagctgatgc gggaaccggg cccactcgtg taggagcggc tgctgaaggc ccgggggcca
                                                                        60
gaggtggaca ccttgtagga cttctgggtc accctgatgg acatggtaga ggctggagtg
                                                                       120
gaggcaggcg ggccgaacca ggcggagatc ct
                                                                       152
<210> 999
<211> 119
<212> DNA
<213> Homo sapien
<220>
<221> misc feature
<222> (1)...(119)
<223> n = A, T, C or G
<400> 999
taaagcaacc actaaaccac ctncagcang agaaagcagc agagagctct tcanacagct
                                                                        60
cagactetga cagetnngag gatgatgaag eteettetaa gecagetggt accaceaag
                                                                       119
<210> 1000
<211> 209
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(209)
<223> n = A, T, C or G
<400> 1000
ccctcnngag gcggagagga tcatgtccgg gaactgcggg gtagtagcga tctgggttac
                                                                        60
ccagccgttg tggcccttga gggtgccacg aagggtcatc tgctcagtca tggcggcggc
                                                                       120
gagagcgtgt gtcgctgcag cgacgaggat ggcactggat ggcttagaga aactagcacc
                                                                       180
acaacetete etgegtegae geggeegeg
                                                                       209
<210> 1001
<211> 390
<212> DNA
<213> Homo sapien
<400> 1001
gtggacacca ccctcaagag cctgagccag cagatcgaga acatccggag cccagagggc
                                                                        60
ageogeaaga acceegeegg cacetgeegt gaceteaaga tgtgceaete tgaetggaag
                                                                       120
agtggagagt actggattga ccccaaccaa ggctgcaacc tggatgccat caaagtcttc
                                                                       180
tgcaacatgg agactggtga gacctgcgtg taccccactc agcccagtgt ggcccagaag
                                                                       240
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	tccagttcga	ccccaaggac gtatggcggc gatgtccacc				300 360 390
<210> 1002 <211> 613 <212> DNA <213> Homo	sapien					
agccgcaaga agtggagagt tgcaacatgg aactggtaca accgatggat cagctgacct aagaacagcg cagggctcca	accecgeceg actggattga agactggtga teagcaagaa teeagttega teetgegeet tggeetacat acgagatega getgeacgag	cctgagccag cacctgcgt ccccaaccaa gacctgcgtg ccccaaggac gtatggcggc gatgtccacc ggaccagcag gatccgcgcc tcacaccgga	gacctcaaga ggctgcaacc taccccactc aagaggcatg cagggctccg gaggcctccc actggcaacc gagggcaaca	tgtgccactc tggatgccat agcccagtgt tctggttcgg accctgccga agaacatcac tcaagaaggc gccgcttcac	tgactggaag caaagtcttc ggcccagaag cgagagcatg tgtggccatc ctaccactgc cctgctcctc ctacagcgtc	60 120 180 240 300 360 420 480 540 600 613
<210> 1003 <211> 639 <212> DNA <213> Homo	sapien					
agccgcaaga agtggagagt tgcaacatgg aactggtaca accgatggat cagctgacct aagaacagcg cagggctcca actgtcgatg	accecgeceg actggattga agactggtga teageaagaa teeagttega teetgegeet tggeetacat acgagatega getgeacgag	cctgagccag cacctgccgt ccccaaccaa gacctgcgtg ccccaaggac gtatggcggc gatgtccacc ggaccagcag gatccgcgcc tcacaccgga gcccatcatc	gacctcaaga ggctgcaacc taccccactc aagaggcatg cagggctccg gaggcctccc actggcaacc gagggcaaca gcctggggca	tgtgccactc tggatgccat agcccagtgt tctggttcgg accctgccga agaacatcac tcaagaaggc gccgcttcac	tgactggaag caaagtcttc ggcccagaag cgagagcatg tgtggccatc ctaccactgc cctgctcctc ctacagcgtc	60 120 180 240 300 360 420 480 540 600 639
<210> 1004 <211> 85 <212> DNA <213> Homo	sapien					
<400> 1004 ccgttattcg ggcctgccgc		agcccggcca gcggg	cgccgccca	agggctcctc	ccgacctccc	60 85
<210> 1005 <211> 636 <212> DNA <213> Homo	sapien					
<400> 1005 gtggacacca agccgcaaga agtggagagt	accccgcccg	cacctgccgt	gacctcaaga	tgtgccactc	tgactggaag	60 120 180

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tgcaacatgg agactggtga gacctgcgtg taccccactc agcccagtgt ggcccagaag
                                                                        240
. aactqqtaca tcaqcaaqaa ccccaaqqac aaqaqqcatq tctqqttcqq cqaqaqcatq
                                                                        300
 accgatggat tecagttega qtatggegge cagggeteeg accetgeega tgtggeeate
                                                                        360
 cagctgacct teetgegeet gatgteeacc gaggeeteec agaacateac etaccactge
                                                                        420
 aagaacagcg tggcctacat ggaccagcaq actggcaacc tcaagaaggc cctgctcctc
                                                                        480
 cagggeteca acqagatega gateeqegee gagggeaaca geegetteae etacagegte
                                                                        540
 actgtcgatg gctgcacgag tcacaccgga gcctggggca agacagtgat tgaatacaaa
                                                                        600
 accaccaaga cctcccqcct qcccatcatc gatqtq
                                                                        636
 <210> 1006
 <211> 629
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature ·
 <222> (1)...(629)
 <223> n = A, T, C or G
 <400> 1006
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                                                                         60
 agccgcaaga accccgcccg cacctgccgt gacctcaaga tgtgccactc tgactggaag
                                                                        120
 agtggagagt actggattga ccccaaccaa ggctgcaacc tggatgccat caaagtcttc
                                                                        180
 tgcaacatgg agactggtga gacctgcgtg taccccactc agcccagtgt ggcccagaag
                                                                        240
 aactggtaca tcagcaagaa ccccaaggac aagaggcatg tctggttcgg cgagagcatg
                                                                        300
 accgatggat tocagttcga gtatggcggc cagggctccg accctgccga tgtggccatc
                                                                        360
 cagetgacet teetgegeet gatgteeace gaggeeteec agaacateae etaceaetge
                                                                         420
 aagaacagcg tggcctacat ggaccagcag actggcaacc tcaagaangc cctgctcctc
                                                                         480
 cagggeteca acgagatega gateegegee gagggeaaca geegetteae etacagegte
                                                                        540
 actgtcgatg gctgcacgag tcacaccgga gcctggggca agacagtgat tgaatacaaa
                                                                         600
                                                                        629
 accaccaaga cctcccgcct gcccatcat
 <210> 1007
 <211> 575
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc feature
 <222> (1)...(575)
 <223> n = A, T, C or G
 <400> 1007
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                                                                          60
                                                                        120
 ageogeaaga acceegeeg cacetgeegt gaceteaaga tgtgeeacte tgactggaag
 agtggagagt actggattga ccccaaccaa ggctgcaacc tggatgccat caaagtcttc
                                                                        180
 tgcaacatgg agactggtga gacctgcgtg taccccactc agcccagtgt ggcccagaag
                                                                        240
                                                                        300
 aactggtnca tcagcaagaa ccccaaggac aagaggcatg tctggttcgg cgagagcatg
                                                                        360
 accgatggat tecagttega gtatggegge cagggeteeg accetgeega tgtggeeate
 cagctgacct tnctgcgcct gatgtccacc gaggcctccc agaacatcac ctaccactgc
                                                                        420
 aagaacagcg tggcctacat ggaccagcag actggcaacc tcaagaaggc cctgctcctc
                                                                        480
 cagggeteca acgagatega gateegegee gagggeaaca geegetteae etacagegte
                                                                        540
 actgtcgatg gctgcacgag tcacaccgga gcctg
                                                                        575
 <210> 1008
 <211> 62
 <212> DNA
 <213> Homo sapien
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<400> 1008 cgatggagcg tgggtaggga gg	gggtccacag	tgtccactcg	ccgtgtgcga	aggttgactc	60 62
<210> 1009 <211> 180 <212> DNA <213> Homo sapien					}
<220> <221> misc_feature <222> (1)(180) <223> n = A,T,C or G					
<400> 1009 gagctgatgc gggaaccggg gaggtggaca ccttgtagga gaggcaggcg ggccgaacca	cttctgggtc	accctgatgg	acatggtaga	ggcaggagtg	60 120 180
<210> 1010 <211> 169 <212> DNA <213> Homo sapien					
<400> 1010 gaggcggcac aggtcacgca tctcgccagg taggtctggg ctcccggatg agaggcaggg	ccaggttctt	gagtttgaag	ctgctggccc	cgctcatgtt cgggcacacg	60 120 169
<210> 1011 <211> 170 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(170) <223> n = A,T,C or G					
<400> 1011 gagctgatgc gggaaccggg gaggtggaca ccttgtanna gaggcaggcg ggccgaacca	cttctgggtc	accctgatgg	acatggtaga	ccgggggcca ggctggagtg	60 120 170
<210> 1012 <211> 344 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1) (344) <223> n = A,T,C or G					
<400> 1012 gtggacacca ccctcaagag agccgcaaga accccgcccg	cctgagccag cacctgccgt	cagatcgaga gacctcaaga	acateeggag tgtgeeacte	cccagagggc tgactggaag	60 120

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agtggagagt actggattga tgcaacatgg agactggtga ctggnncatc ngcangaacc cnatggattc canttnnagt	gacctgcgtg ccnnggacan	taccccactc gaggcntgtc	agcccagtgg tggttcggcg	nccanaanaa	180 240 300 344
<210> 1013 <211> 157 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(157) <223> n = A,T,C or G					
<400> 1013 atagaacccc gcccgcacct agagtactgg attgacccca catgganact ggtganncct	accaaggctg	caacctggat			60 120 157
<210> 1014 <211> 621 <212> DNA <213> Homo sapien					
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<210> 1015 <211> 104 <212> DNA <213> Homo sapien					
<220> <221> misc_feature <222> (1)(104) <223> n = A,T,C or G					
<400> 1015 gtggacacca ccctcaagag agccgcaaga accccgcccg				cccagagggc	60 104
<210> 1016 <211> 101 <212> DNA <213> Homo sapien					
<400> 1016					

		agctgcccat gagatgtgga			ggatccctgg	60 101
<210> 1017 <211> 172 <212> DNA <213> Homo	sapien					
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tgccgggcag gggaaggagg aggtgctctt cgagctgttg gtgtccaggg cactgggaat
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cgcagcette cagcectega aateggtgae gtetgecaeg aagageeett egeagageat
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tttttccttc caatcagggg ctcgctcttc tgattattct tcagggcaat gacataaatt
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teacecaget ageteaaaca accatgagat cagagetegg caaactetet etggacaaag
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tgaaagagtc tatgcagatg cangtggagg cagagcggcg gaaacgggcc acagttctag
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  catgaaaaca aatggtctgt aatcttataa accaacatag catttcactg tcaacaatgt
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· gaaaatttaa tatettetea aacaggeata agatgaagaa gtgetatttt ttaattgtaa
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301

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<400> 1059

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Glu Asn Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu 20 25 30

Asp Asn Thr Asn Glu Tyr Asn Ser Asn Asp Gly Lys Lys Leu Pro Gln 35 40 45

Gly Glu Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu 50 55 60

Cys Asn Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe 65 70 75 80

Thr Glu Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu 85 90 95

Met Arg Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val 100 105 110

<211> 440

<212> PRT

<213> Homo sapiens

Leu	Lys	Ala 115	Ser	Arg	Glu	Glu	Lys 120	Val	Leu	Met	Asp	Glu 125	Gly	Ala	Val
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Gln 145	Trp	Ser	Asn	Val	Phe 150	Asn	Ile	Leu	Arg	Glu 155	Asn	Asp	Phe	Glu	Pro 160
Lys	Phe	Leu	Cys	Glu 165	Val	Lys	Leu	Ala	Phe 170	Lys	Cys	Asp	Gly	Glu 175	Ile
Lys	Thr	Phe	Ser 180	Asp	Leu	Gln	Ser	Leu 185	Arg	Lys	Phe	Ala	Ser 190	Gln	Ьys
Ser	Ser	Met 195	Lys	Glu	Leu	Leu	Lys 200	qaA,	Val	Leu	Pro	Gln 205	Гуs	Glu	Glu
Ile	Asn 210	Gln	Gly	Gly	Arg	Lys 215	Tyr	Gly	Ile	Gln	Glu 220	Lys	Arg	Asp	Lys
Thr 225	Leu	Ile	Asp	Ser	Lys 230	His	Arg	Ala	Gly	Glu 235	Ile	Thr	Ser	Asp	Gl ₃ 240
Leu	Ser	Phe	Leu	Phe 245	Leu	Lys	Glu	Val	Lys 250	Val	Ala	Lys	Pro	Glu 255	Glu
Met	Lys	Asn	Leu 260	Glu	Thr	Gln	Glu	Glu 265	Glu	Phe	Ser	Glu	Leu 270	Glu	Glu
Leu	Asp	Glu 275		Ala	Ser	Gly	Met 280	Glu	Asp	Asp	Glu	Asp 285	Thr	Ser	G13
Leu	Glu 290	Glu	Glu	Glu	Glu	Glu 295	Pro	Ser	Gly	Leu	Glu 300	Glu	Glu	Glu	Glu
Glu 305	Glu	Ala	Ser	Gly	Leu 310	Glu	Glu	Asp	Glu	Ala 315	Ser	Gly	Leu	Glu	Glu 320
Glu	Glu	Glu	Gln	Thr 325	Ser	Glu	Gln	Asp	Ser 330	Thr	Phe	Gln	Gly	His 335	Thr
Leu	Val	Asp	Ala 340				Val			Thr	Ser	Asp	Gly 350		Glu
Thr	Thr	Phe 355	Ile	Asp	Ser	Val	Glu 360	Asp	Ser	Glu	Ser	Glu 365	Glu	Glu	Glu
Glu	Gly 370	Lys	Ser	Ser	Glu	Thr 375	Gly	Lys	Val	Lys	Thr 380	Thr	Ser	Leu	Thr
Glu 385	Гàз	Lys	Ala	Ser	Arg 390	Arg	Gln	Lys	Glu	Ile 395	Pro	Phe	Ser	Tyr	Leu 400
Val	Gly	Asp	Ser	Gly 405	Lys	Lys	Lys	Leu	Val 410	Lys	His	Gln	Val	Val 415	His

304

Lys Thr Gln Glu Glu Glu Glu Thr Ala Val Pro Thr Ser Gln Gly Thr
420 425 430

Gly Thr Pro Cys Leu Thr Leu Cys 435 440

<210> 1060

<211> 230

<212> PRT

<213> Homo sapiens

<400> 1060

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Trp Met Ala Ala Cys Met Leu Ala Ser Lys Gly Lys Thr Met Ala Asp
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Ser Ser Tyr Gln Pro Glu Val Leu Asn Ile Leu Ser Phe Leu Arg Met 35 40 45

Lys Asn Arg Asn Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn Met 50 55 60

Asp Met Asn Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Arg His 65 70 75 80

Lys Ser Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn Val 85 90 95

Ala Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala Trp
100 105 110

Gln Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe Lys 115 120 125

Gly Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg Leu Ile 130 135 140

Lys Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp Arg Phe Thr 145 150 155 160

Asn Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg Gln Val Val Ile 165 170 175

Glu Phe Asp Gln Asn Val Phe Thr Ala Phe Thr Cys Leu Ser Ala Asp 180 185 190

Cys Lys Ile Val His Glu Tyr Ile Gly Gly Tyr Ile Phe Leu Ser Thr 195 200 205

Arg Ser Lys Asp Gln Asn Glu Thr Leu Asp Glu Asp Leu Phe His Lys 210 . 215 220

Leu Thr Gly Gly Gln Asp 225 230

PCT/US00/35596 WO 01/49716

305

<210> 1061 <211> 311

<212> PRT

<213> Homo sapiens

<400> 1061

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Ser Val Arg His Ser Gly Gly Leu Asn Leu Ala Pro Gln Asn Phe Val

Ser Pro Pro Gln Tyr Pro Asp Tyr Gly Gly Tyr His Val Ala Ala Ala

Ala Ala Gln Asn Leu Asp Ser Ala Gln Ser Pro Gly Pro Ser Trp

Pro Ala Ala Tyr Gly Ala Pro Leu Arg Glu Asp Trp Asn Gly Tyr Ala

Pro Gly Gly Ala Ala Ala Ala Asn Ala Val Ala His Ala Leu Asn Gly

Gly Ser Pro Ala Ala Ala Met Gly Tyr Ser Ser Pro Ala Asp Tyr His

Pro His His Pro His His Pro His His Pro Ala Ala Pro

Ser Cys Ala Ser Gly Leu Leu Gln Thr Leu Asn Pro Gly Pro Pro Gly

Pro Ala Ala Thr Ala Ala Ala Glu Gln Leu Ser Pro Gly Gly Gln Arg

Arg Asn Leu Cys Glu Trp Met Arg Lys Pro Ala Gln Gln Ser Leu Gly 170

Ser Gln Val Lys Thr Arg Thr Lys Asp Lys Tyr Arg Val Val Tyr Thr 185

Asp His Gln Arg Leu Glu Leu Glu Lys Glu Phe His Tyr Ser Arg Tyr

Ile Thr Ile Arg Arg Lys Ala Glu Leu Ala Ala Thr Leu Gly Leu Ser

Glu Arg Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Ala Lys Glu Arg

Lys Ile Asn Lys Lys Leu Gln Gln Gln Gln Gln Gln Pro Pro 250

Gln Pro Pro Pro Pro Pro Gln Pro Gln Pro Gln Pro Gly Pro 265

PCT/US00/35596 WO 01/49716

306

Leu Arg Ser Val Pro Glu Pro Leu Ser Pro Val Ser Ser Leu Gln Ala

Ser Val Ser Gly Ser Val Pro Gly Val Leu Gly Pro Thr Gly Gly Val 295

Leu Asn Pro Thr Val Thr Gln

<210> 1062

<211> 237

<212> PRT

<213>- Homo sapiens

<400> 1062

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Phe Leu Phe Trp Leu Cys Gly Ile Leu Ile Leu Ala Leu Ala Ile Trp

Val Arg Val Ser Asn Asp Ser Gln Ala Ile Phe Gly Ser Glu Asp Val

Gly Ser Ser Ser Tyr Val Ala Val Asp Ile Leu Ile Ala Val Gly Ala 55

Ile Ile Met Ile Leu Gly Phe Leu Gly Cys Cys Gly Ala Ile Lys Glu

Ser Arg Cys Met Leu Leu Leu Phe Phe Ile Gly Leu Leu Leu Ile Leu

Leu Leu Gln Val Ala Thr Gly Ile Leu Gly Ala Val Phe Lys Ser Lys

Ser Asp Arg Ile Val Asn Glu Thr Leu Tyr Glu Asn Thr Lys Leu Leu 120

Ser Ala Thr Gly Glu Ser Glu Lys Gln Phe Gln Glu Ala Ile Ile Val

Phe Gln Glu Glu Phe Lys Cys Cys Gly Leu Val Asn Gly Ala Ala Asp

Trp Gly Asn Asn Phe Gln His Tyr Pro Glu Leu Cys Ala Cys Leu Asp

Lys Gln Arg Pro Cys Gln Ser Tyr Asn Gly Lys Gln Val Tyr Lys Glu 180 185 190

Thr Cys Ile Ser Phe Ile Lys Asp Phe Leu Ala Lys Asn Leu Ile Ile 200

Val Ile Gly Ile Ser Phe Gly Leu Ala Val Ile Glu Ile Leu Gly Leu 215

307

Val Phe Ser Met Val Leu Tyr Cys Gln Ile Gly Asn Lys 225 230 235

<210> 1063

<211> 80

<212> PRT

<213> Homo sapiens

<400> 1063

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Ala Val Pro Ala Lys Asp Arg Val Asp Cys Gly Tyr Pro His Val Thr 35 40 45

Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys Phe Asp Ser Arg Ile Pro 50 55 60

Gly Val Pro Trp Cys Phe Lys Pro Leu Gln Glu Ala Glu Cys Thr Phe 65 70 75 80

<210> 1064

<211> 323

<212> PRT

<213> Homo sapiens .

<400> 1064

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Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser 20 25 30

Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val 35 40 45

Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe 50 55 60

Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln 65 70 75 80

Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys 85 90 95

Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr 100 105 110

Lys Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu 115 120 125

Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu 130 135 140

308

Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro 145 150 155 160

Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu 165 170 175

Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val 180 185 190

Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile 195 200 205

Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn 210 215 220

Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg 225 230 235 240

Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp 245 250 255

Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln 260 265 270

Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr 275 280 285

Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe 290 295 300

Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr 305 310 315 320

Val Gln Ile

<210> 1065

<211> 957

<212> PRT

<213> Homo sapiens

<400> 1065

Arg Asn Arg Pro His Thr Thr Ala Phe Pro Gly Ser Thr Thr Met Pro

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Gly Val Ser Gln Glu Ser Thr Ala Ser His Ser Ser Pro Gly Ser Thr 20 25 30

Asp Thr Thr Leu Ser Pro Gly Ser Thr Thr Ala Ser Ser Leu Gly Pro 35 40

Glu Ser Thr Thr Phe His Ser Gly Pro Gly Ser Thr Glu Thr Thr Leu 50 60

Leu Pro Asp Asn Thr Thr Ala Ser Gly Leu Leu Glu Ala Ser Thr Pro 65 70 75 80

Val	His	Ser	Ser	Thr 85	Gly	Ser	Pro	His	Thr 90	Thr	Leu	Ser	Pro	Ala 95	Gly
Ser	Thr	Thr	Arg 100	Gln	Gly	Glu	Ser	Thr 105	Thr	Phe	Gln	Ser	Trp 110	Pro	Asn
Ser	Lys	Asp 115	Thr	Thr	Pro	Ala	Pro 120	Pro	Thr	Thr	Thr	Ser 125	Ala	Phe	Val
Glu	Leu 130	Ser	Thr	Thr	Ser	His 135	Gly	Ser	Pro	Ser	Ser 140	Thr	Pro	Thr	Thr
His 145	Phe	Ser	Ala	Ser	Ser 150	Thr	Thr	Leu	Gly	Arg 155	Ser	Glu	Glu	Ser	Thr 160
Thr	Val	His	Ser	Ser 165	Pro	Val	Ala	Thr	Ala 170	Thr	Thr	Pro	Ser	Pro 175	Ala
Arg	Ser	Thr	Thr 180	Ser	Gly	Leu	Val	Glu 185	Glu	Ser	Thr	Thr	Tyr 190	His	Ser
Ser	Pro	Gly 195	Ser	Thr	Gln	Thr	Met 200	His	Phe	Pro	Glu	Ser 205	Asp	Thr	Thr
Ser	Gly 210	Arg	Gly	Glu	Glu	Ser 215	Thr	Thr	Ser	His	Ser 220	Ser	.Thr	Thr	His
Thr 225	Ile	Ser	Ser	Ala	Pro 230	Ser	Thr	Thr	Ser	Ala 235	Leu	Val	Glu	Glu	Pro 240
Thr	Ser	Tyr	His	Ser 245	Ser	Pro	Gly	Ser	Thr 250	Ala	Thr	Thr	His	Phe 255	Pro
Asp	Ser	Ser	Thr 260	Thr	Ser	Gly	Arg	Ser 265	Glu	Glu	Ser	Thr	Ala 270	Ser	His
Ser	Asn	Gln 275	Asp	Ala	Thr	Gly	Thr 280	Ile	Val	Leu	Pro	Ala 285	Arg	Ser	Thr
Thr	Ser 290	Val	Leu	Leu	Gly	Glu 295	Ser	Thr	Thr	Ser	Pro 300	Ile	Ser	Ser	Gly
Ser 305	Met	Glu	Thr	Thr	Ala 310	Leu	Pro	Gly ·	Ser	Thr 315	Thr	Thr	Pro	Gly	Leu 320
Ser	Glu	Lys	Ser	Thr 325		Phe	His	Ser	Ser 330	Pro	Arg	Ser	Pro	Ala 335	Thr
Thr	Leu	Ser	Pro 340	Ala	Ser	Thr	Thr	Ser 345	Ser	Gly	Val	Ser	Glu 350	Glu	Ser
Thr	Thr	Ser 355	His	Ser	Arg	Pro	Gly 360	Ser	Thr	His	Thr	Thr 365	Ala	Phe	Pro
Asp	Ser	Thr	Thr	Thr	Pro	Gly 375		Ser	Arg	His	Ser 380		Thr	Ser	His

Ser Ser Pro Gly Ser Thr Asp Thr Thr Leu Leu Pro Ala Ser Thr Thr Thr Ser Gly Pro Ser Gln Glu Ser Thr Thr Ser His Ser Ser Pro Gly 410 Ser Thr Asp Thr Ala Leu Ser Pro Gly Ser Thr Thr Ala Leu Ser Phe 425 Gly Glu Ser Thr Thr Phe His Ser Ser Pro Gly Ser Thr His Thr 440 Thr Leu Phe Pro Asp Ser Thr Thr Ser Ser Gly Ile Val Glu Ala Ser 455 Thr Arg Val His Ser Ser Thr Gly Ser Pro Arg Thr Thr Leu Ser Pro Ala Ser Ser Thr Ser Pro Gly Leu Gln Gly Glu Ser Thr Ala Phe Gln 485 490 Thr His Pro Ala Ser Thr His Thr Thr Pro Ser Thr Pro Ser Thr Ala 505 Thr Ala Pro Val Glu Glu Ser Thr Thr Tyr His Arg Ser Pro Ser Ser 520 Thr Pro Thr Thr His Phe Pro Ala Ser Ser Thr Thr Ser Gly His Ser 535 Glu Lys Ser Thr Ile Phe His Ser Ser Pro Asp Ala Ser Gly Thr Thr 550 Pro Ser Ser Ala His Ser Thr Thr Ser Gly Arg Gly Glu Ser Thr Thr 570 Ser Arg Ile Ser Pro Gly Ser Thr Glu Ile Thr Thr Leu Pro Gly Ser Thr Thr Pro Gly Leu Ser Glu Ala Ser Thr Thr Phe Tyr Ser Ser Pro Arg Ser Pro Thr Thr Thr Leu Ser Pro Ala Ser Met Thr Ser Leu 61.5 Gly Val Gly Glu Glu Ser Thr Thr Ser Arg Ser Gln Pro Gly Ser Thr 630 635 His Ser Thr Val Ser Pro Ala Ser Thr Thr Thr Pro Gly Leu Ser Glu 650 Glu Ser Thr Thr Val Tyr Ser Ser Pro Gly Ser Thr Glu Thr Thr Val Phe Pro Arg Ser Thr Thr Thr Ser Val Arg Gly Glu Glu Pro Thr Thr Phe His Ser Arg Pro Ala Ser Thr His Thr Thr Leu Phe Thr Glu 311

690 695 700 Asp Ser Thr Thr Ser Gly Leu Thr Glu Glu Ser Thr Ala Phe Pro Gly 710 Ser Pro Ala Ser Thr Gln Thr Gly Leu Pro Ala Thr Leu Thr Thr Ala 730 Asp Leu Gly Glu Glu Ser Thr Thr Phe Pro Ser Ser Ser Gly Ser Thr 745 Gly Thr Thr Leu Ser Pro Ala Arg Ser Thr Thr Ser Gly Leu Val Gly 760 Glu Ser Thr Pro Ser Arg Leu Ser Pro Ser Ser Thr Glu Thr Thr Leu Pro Gly Ser Pro Thr Thr Pro Ser Leu Ser Glu Lys Ser Thr Thr Phe Tyr Thr Ser Pro Arg Ser Pro Asp Ala Thr Leu Ser Pro Ala Thr 810 Thr Thr Ser Ser Gly Val Ser Glu Glu Ser Ser Thr Ser His Ser Gln 825 Pro Gly Ser Thr His Thr Thr Ala Phe Pro Asp Ser Thr Thr Thr Ser 840 Gly Leu Ser Gln Glu Pro Lys Thr Ser His Ser Ser Gln Gly Ser Thr Glu Ala Thr Leu Ser Pro Gly Ser Thr Thr Ala Ser Ser Leu Gly Gln Gln Ser Thr Thr Phe His Ser Ser Pro Gly Asp Thr Glu Thr Thr Leu 890 Leu Pro Asp Asp Thr Ile Thr Ser Gly Leu Val Glu Ala Ser Thr Pro Thr His Ser Ser Thr Gly Ser Leu His Thr Thr Leu Thr Pro Ala Ser 920 Ser Thr Ser Ala Gly Leu Gln Glu Glu Ser Thr Thr Phe Gln Ser Trp 935 Pro Ser Ser Ser Asp Thr Thr Pro Ser Pro Pro Gly Pro 950 <210> 1066 <211> 914 <212> PRT <213> Homo sapiens

Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu

<400> 1066

312

				5					10					15	
Glu	Gly	Ala	Leu 20	Ser	Asn	Ser	Leu	Ile 25	Gln	Leu	Asn	Asn	Asn 30	Gly	Tyr
Glu	Gly	Ile 35	Val	Val	Ala	Ile	Asp 40	Pro	Asn	Val	Pro	Glu 45	Asp	Glu	Thr
Leu	Ile 50	Gln	Gln	Ile	Lys	Asp 55	Met	Val	Thr	Gln	Ala 60	Ser	Leu	Tyr	Leu
Phe 65	Glu	Ala	Thr	Gly	Lys 70	Arg	Phe	Tyr	Phe	Lys 75	Asn	Val	Ala	Ile	Leu 80
Ile	Pro	Glu	Thr	Trp 85	ГÀЗ	Thr	Lys	Ala	Asp 90	Tyr	Val	Arg	Pro	Lys 95	Leu
Glu	Thr	Tyr	Lys 100	Asn	Ala	Asp	Val	Leu 105	Val	Ala	Glu	Ser	Thr 110	Pro	Pro
Gly	Asn	Asp 115	Glu	Pro	Tyr	Thr	Glu 120	Gln	Met	Gly	Asn.	Cys 125	Gly	Glu	Lys
Gly	Glu 130	Arg	Ile	His	Leu	Thr 135	Pro	Asp	Phe	Ile	Ala 140	Gly	Lys	Lys	Leu
Ala 145	Glu	Tyr	Gly	Pro	Gln 150	Gly	Lys	Ala	Phe	Val 155	His	Glu	Trp	Ala	His 160
Leu	Arg	Trp	Gly	Val 165	Phe	Asp	Glu	Tyr	Asn 170	Asn	Asp	Glu	ГÀЗ	Phe 175	Туг
Leu	Ser	Asn	Gly 180	Arg	Ile	Gln	Ala	Val 185	Arg	Cys	Ser	Ala	Gly 190	Ile	Thr
Gly	Thr	Asn 195	Val	Val	Lys	Lys	Cys 200	Gln	Gly	Gly	Ser	Cys 205	Tyr	Thr	Ьys
Arg	Cys 210	Thr	Phe	Asn	Lys	Val 215	Thr	Gly	Leu	Tyr	Glu 220	Lys	Gly	Суѕ	Glu
Phe 225	Val	Leu	Gln	Ser	Arg 230	Gln	Thr	Glu	Lys	Ala 235	Ser	Ile	Met	Phe	Ala 240
Gln	His	Val	Asp	Ser 245	Ile	Val	Glu	Phe	Cys 250	Thr	Glu	Gln	Asn	His 255	Asn
Lys	Glu	Ala	Pro 260	Asn	Lys	Gln	Asn	Gln 265	ГÀЗ	Суз	Asn	Leu	Arg 270	Ser	Thr
Trp	Glu	Val 275	Ile	Arg	Asp	Ser	Glu 280	Asp	Phe	Lys	Lys	Thr 285	Thr	Pro	Met
Thr	Thr 290	Gln	Pro	Pro	Asn	Pro 295	Thr	Phe	Ser	Leu	Leu 300	Gln	Ile	Gly	Gln
Arg 305	Ile	Val	Cys	Leu	Val 310	Leu	Asp	Lys	Ser	Gly 315	Ser	Met	Ala	Thr	Gly 320

Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile 425 His Thr Val Ala Leu Gly Pro Ser Ala Ala Gln Glu Leu Glu Glu Leu 440 Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln 455 Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln Ile Leu Leu Trp Asp Pro Ser Gly Gln Lys Gln Gly Gly Phe Val Val Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys 550 555 Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr 570 Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu

Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala

Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly 650 Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro 745 Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro 810 Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu 855 Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr 865 870 Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile 890 His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser

Ile Ala

<210> 1067 <211> 585 <212> PRT <213> Homo sapiens <400> 1067 Thr Leu Ser Pro Ala Ser Met Arg Ser Ser Ser Ile Ser Gly Glu Pro Thr Ser Leu Tyr Ser Gln Ala Glu Ser Thr His Thr Thr Ala Phe Pro Ala Ser Thr Thr Thr Ser Gly Leu Ser Gln Glu Ser Thr Thr Phe His Ser Lys Pro Gly Ser Thr Glu Thr Thr Leu Ser Pro Gly Ser Ile Thr 55 Thr Ser Ser Phe Ala Gln Glu Phe Thr Thr Pro His Ser Gln Pro Gly Ser Ala Leu Ser Thr Val Ser Pro Ala Ser Thr Thr Val Pro Gly Leu Ser Glu Glu Ser Thr Thr Phe Tyr Ser Ser Pro Gly Ser Thr Glu Thr Thr Ala Phe Ser His Ser Asn Thr Met Ser Ile His Ser Gln Gln Ser 120 Thr Pro Phe Pro Asp Ser Pro Gly Phe Thr His Thr Val Leu Pro Ala Thr Leu Thr Thr Asp Ile Gly Gln Glu Ser Thr Ala Phe His Ser 155 Ser Ser Asp Ala Thr Gly Thr Thr Pro Leu Pro Ala Arg Ser Thr Ala 170 Ser Asp Leu Val Gly Glu Pro Thr Thr Phe Tyr Ile Ser Pro Ser Pro 185 Thr Tyr Thr Thr Leu Phe Pro Ala Ser Ser Ser Thr Ser Gly Leu Thr Glu Glu Ser Thr Thr Phe His Thr Ser Pro Ser Phe Thr Ser Thr Ile Val Ser Thr Glu Ser Leu Glu Thr Leu Ala Pro Gly Leu Cys Gln Glu

Gly Gln Ile Trp Asn Gly Lys Gln Cys Val Cys Pro Gln Gly Tyr Val
245
250
255

Gly Tyr Gln Cys Leu Ser Pro Leu Glu Ser Phe Pro Val Glu Thr Pro

235

230

Gly Tyr Gln Cys Leu Ser Pro Leu Glu Ser Phe Pro Val Glu Thr Pro 260 265 270

Glu Lys Leu Asn Ala Thr Leu Gly Met Thr Val Lys Val Thr Tyr Arg

PCT/US00/35596

316

		275					280					285			
Asn	Phe 290	Thr	Glu	Lys	Met	Asn 295	Asp	Ala	Ser	Ser	Gln 300	Glu	Tyr	Gln	Asn
Phe 305	Ser	Thr	Leu	Phe	Lys 310	Asn	Arg	Met	Asp	Val 315	Val	Leu	Lys	Gly	Asp 320
Asn	Leu	Pro	Gln	Tyr 325	Arg	Gly	Val	Asn	Ile 330	Arg	Arg	Leu	Leu	Asn 335	Gly
Ser	Ile	Val	Val 340	Lys	Asn	Asp	Val	Ile 345	Leu	Glu	Ala	Asp	Tyr 350	Thr	Leu
Glu	Tyr	Glu 355	Glu	Leu	Phe	Glu	Asn 360	Leu	Ala	Glu	Ile	Val 365	Lys	Ala	Lys
Ile	Met 370	Asn	Glu	Thr	Arg	Thr 375	Thr	Leu	Leu	Asp	Pro 380	Asp	Ser	Cys	Arg
Lys 385	Ala	Ile	Leu	Сув	Tyr 390	Ser	Glu	Glu	Asp	Thr 395	Phe	Val	Asp	Ser	Ser 400
Val	Thr	Pro	Gly	Phe 405	Asp	Phe	Gln	Glu	Gln 410	Cys	Thr	Gln	Lys	Ala 415	Ala
Glu	Gly	Tyr	Thr 420	Gln	Phe	Tyr	Tyr	Val 425	Asp	Val	Leu	Asp	Gly 430	Lys	Leu
Ala	Суз	Val 435	Asn	Lys	Суз	Thr	Lys 440	Gly	Thr	Lys	Ser	Gln 445	Met	Asn	Суз
Asn	Leu 450	Gly	Thr	Сув	Gln	Leu 455	Gln	Arg	Ser	Gly	Pro 460	Arg	Cys	Leu	Cys
Pro 465	Asn	Thr	Asn _,	Thr	His 470	Trp	Tyr	Trp	Gly	Glu 475	Thr	Суз	Glu	Phe	Asn 480
Ile	Ala	Lys	Ser	Leu 485	Val	Tyr	Gly	Ile	Val 490	Glу	Ala	Val	Met	Ala 495	Val
Leu	Leu	Leu	Ala 500	Leu	Ile	Ile	Leu	Ile 505	Ile	Leu	Phe	Ser	Leu 510	Ser	Gln
Arg	Lys	Arg 515	His	Arg	Glu	Gln	Tyr 520	Asp	Val	Pro	Gln	Glu 525	Trp	Arg	ГЛЗ
Glu	Gly 530	Thr	Pro	Gly	Ile	Phe 535	Gln	Lys	Thr	Ala	Ile 540	Trp	Glu	Asp	Gln
Asn 545	Leu	Arg	Glu	Ser	Arg 550	Phe	Gly	Leu	Glu	Asn 555	Ala	Tyr	Asn	Asn	Phe 560
Arg	Pro	Thr	Leu	Glu 565	Thr	Val	Asp	Ser	Gly 570	Thr	Glu	Leu	His	Ile 575	Gln
Arg	Pro	Glu	Met 580	Val	Ala	Ser	Thr	Val 585							

317

<210> 1068 <211> 5179 <212> PRT <213> Homo sapiens <400> 1068 Met Gly Leu Pro Leu Ala Arg Leu Ala Ala Val Cys Leu Ala Leu Ser Leu Ala Gly Gly Ser Glu Leu Gln Thr Glu Gly Arg Thr Arg Tyr His Gly Arg Asn Val Cys Ser Thr Trp Gly Asn Phe His Tyr Lys Thr Phe Asp Gly Asp Val Phe Arg Phe Pro Gly Leu Cys Asp Tyr Asn Phe Ala Ser Asp Cys Arg Gly Ser Tyr Lys Glu Phe Ala Val His Leu Lys Arg 70 Gly Pro Gly Gln Ala Glu Ala Pro Ala Gly Val Glu Ser Ile Leu Leu Thr Ile Lys Asp Asp Thr Ile Tyr Leu Thr Arg His Leu Ala Val Leu Asn Gly Ala Val Val Ser Thr Pro His Tyr Ser Pro Gly Leu Leu Ile Glu Lys Ser Asp Ala Tyr Thr Lys Val Tyr Ser Arg Ala Gly Leu Thr 135 Leu Met Trp Asn Arg Glu Asp Ala Leu Met Leu Glu Leu Asp Thr Lys Phe Arg Asn His Thr Cys Gly Leu Cys Gly Asp Tyr Asn Gly Leu Gln Ser Tyr Ser Glu Phe Leu Ser Asp Gly Val Leu Phe Ser Pro Leu Glu 180 185 Phe Gly Asn Met Gln Lys Ile Asn Gln Pro Asp Val Val Cys Glu Asp Pro Glu Glu Val Ala Pro Ala Ser Cys Ser Glu His Arg Ala Glu Cys Glu Arg Leu Leu Thr Ala Glu Ala Phe Ala Asp Cys Gln Asp Leu Val Pro Leu Glu Pro Tyr Leu Arg Ala Cys Gln Gln Asp Arg Cys Arg Cys Pro Gly Gly Asp Thr Cys Val Cys Ser Thr Val Ala Glu Phe Ser

265

260

Arg	Gln	Суз 275	Ser	His	Ala	Gly	Gly 280	Arg	Pro	Gly	Asn	Trp 285	Arg	Thr	Ala
Thr	Leu 290	Суз	Pro	Lys	Thr	Cys 295	Pro	Gly	Asn	Leu	Val 300	Tyr	Leu	Glu	Ser
Gly 305	Ser	Pro	Суз	Met	Asp 310	Thr	Суз	Ser	His	Leu 315	Glu	Val	Ser	Ser	Leu 320
Cys	Glu	Glu	His	Arg 325	Met	Asp	Gly	Суз	Phe 330	Суз	Pro	Glu	Gly	Thr 335	Val
Tyr	Asp	Asp	Ile 340	Gly	Asp	Ser	Gly	Cys 345	Val	Pro	Val	Ser	Gln 350	Суѕ	His
Cys	Arg	Leu 355	His	Gly	His	Leu	Tyr 360	Thr	Pro	Gly	Gln	Glu 365	Ile	Thr	Asn
Asp	Cys 370	Glu	Gln	Суѕ	Val	Cys 375	Asn	Ala	Gly	Arg	Trp 380	Val	Суз	Lys	Asp
Leu 385	Pro	Суѕ	Pro	Gly	Thr 390	Суз	Ala	Leu	Glu	Gly 395	Gly	Ser	His	Ile	Thr 400
Thr	Phe	Asp	Gly	Lys 405	Thr	Tyr	Thr	Phe	His 410	Gly	Asp	Сув	Tyr	Tyr 415	Val
Leu	Ala	Lys	Gly 420	Asp	His	Asn	Asp	Ser 425	Tyr	Ala	Leu	Leu	Gly 430	Glu	Leu
Ala	Pro	<i>Cys</i> 435	Gly	Ser	Thr	Asp	Lys 440	Gln	Thr	Cys	Leu	Lys 445	Thr	Val	Val
Leu	Leu 450	Ala	Asp	Lys	Lys	Lys 455	Asn	Ala	Val	Val	Phe 460	Lys	Ser	Asp	Gly
Ser 465	Val	Leu	Leu	Asn	Gln 470	Leu	Gln	Val	Asn	Leu 475	Pro	His	Val	Thr	Ala 480
Ser	Phe	Ser	Val	Phe 485	Arg	Pro	Ser	Ser	Tyr 490	His	Ile	Met	Val	Ser 495	Met
Ala	Ile	Gly	Val 500	Arg	Leu	Gln	Val.	Gln 505	Leu	Ala	Pro	Val	Met 510	Gln	Leu
Phe	Val	Thr 515	Leu	Asp	Gln	Ala	Ser 520	Gln	Gly	Gln	Val	Gln 525	Gly	Leu	Суз
Gly	Asn 530	Phe	Asn	Gly	Leu	Glu 535	Gly	Asp	Asp	Phe	Lys 540	Thr	Ala	Ser	Gly
Leu 545	Val	Glu	Ala	Thr	Gly 550	Ala	Gly	Phe	Ala	Asn 555	Thr	Trp	Lys	Ala	Gln 560
Ser	Thr	Cys	His	Asp 565	Lys	Leu	Asp	Trp	Leu 570	Asp	Asp	Pro	Cys	Ser 575	Leu

Asn Ile Glu Ser Ala Asn Tyr Ala Glu His Trp Cys Ser Leu Leu Lys Lys Thr Glu Thr Pro Phe Gly Arg Cys His Ser Ala Val Asp Pro Ala Glu Tyr Tyr Lys Arg Cys Lys Tyr Asp Thr Cys Asn Cys Gln Asn Asn Glu Asp Cys Leu Cys Ala Ala Leu Ser Ser Tyr Ala Arg Ala Cys Thr 630 Ala Lys Gly Val Met Leu Trp Gly Trp Arg Glu His Val Cys Asn Lys Asp Val Gly Ser Cys Pro Asn Ser Gln Val Phe Leu Tyr Asn Leu Thr Thr Cys Gln Gln Thr Cys Arg Ser Leu Ser Glu Ala Asp Ser His Cys Leu Glu Gly Phe Ala Pro Val Asp Gly Cys Gly Cys Pro Asp His Thr 695 Phe Leu Asp Glu Lys Gly Arg Cys Val Pro Leu Ala Lys Cys Ser Cys Tyr His Arg Gly Leu Tyr Leu Glu Ala Gly Asp Val Val Arg Gln Glu Glu Arg Cys Val Cys Arg Asp Gly Arg Leu His Cys Arg Gln Ile Arg Leu Ile Gly Gln Ser Cys Thr Ala Pro Lys Ile His Met Asp Cys Ser Asn Leu Thr Ala Leu Ala Thr Ser Lys Pro Arg. Ala Leu Ser Cys Gln Thr Leu Ala Ala Gly Tyr Tyr His Thr Glu Cys Val Ser Gly Cys Val Cys Pro Asp Gly Leu Met Asp Asp Gly Arg Gly Gly Cys Val Val 810 Glu Lys Glu Cys Pro Cys Val His Asn Asn Asp Leu Tyr Ser Ser Gly Ala Lys Ile Lys Val Asp Cys Asn Thr Cys Thr Cys Lys Arg Gly Arg Trp Val Cys Thr Gln Ala Val Cys His Gly Thr Cys Ser Ile Tyr Gly Ser Gly His Tyr Ile Thr Phe Asp Gly Lys Tyr Tyr Asp Phe Asp Gly His Cys Ser Tyr Val Ala Val Gln Asp Tyr Cys Gly Gln Asn Ser Ser

320

				885					890					895	
Leu	G1y	Ser	Phe 900	Ser	Ile	Ile	Thr	Glu 905	Asn	Val	Pro	Суз	Gly 910	Thr	Thr
Gly	Val	Thr 915	Cys	Ser	Lys	Ala	Ile 920	Lys	Ile	Phe	Met	Gly 925	Arg	Thr	Glu
Leu	Lys 930	Leu	Glu	Asp	ГАЗ	His 935	Arg	Val	Val	Ile	Gln 940	Arg	Asp	Glu	Gly
His 945	His	Val	Ala	Tyr	Thr 950	Thr	Arg	Glu	Val	Gly 955	Gln	Tyr	Leu	Val	Val 960
Glu	Ser	Ser	Thr	Gly 965	Ile	Ile	Val	Ile	Trp 970	Asp	Lys	Arg	Thr	Thr 975	Val
Phe	Ile	Lys	Leu 980	Ala	Pro	Ser	Tyr	Lys 985	Gly	Thr	Val	Суѕ	Gly 990	Leụ	Cys
Gly	Asn	Phe 995	Asp	His	Arg	Ser	Asn 100		Asp	Phe	Thr	Thr 100		Asp	His
Met	Val 1010		Ser	Ser	Glu	Leu 101		Phe	Gly	Asn	Ser 102	_	Lys	Glu	Ala
Pro 102		Суз	Pro	Asp	Val 1030		Thr	Asn	Pro	Glu 103		Cys	Ser	Leu	Asn 1040
Pro	His	Arg	Arg	Ser 104		Ala	Glu	Lys	Gln 105	Cys O	Ser	Ile	Leu	Lys 105	
Ser	Val	Phe	Ser 106		Cys	His	Ser	Lys 106		Asp	Pro	Lys	Pro 1070		Tyr
Glu	Ala	Cys 107		His	Asp	Ser	Cys 1080		Cys	Asp	Thr	Gly 108		Asp	Cys
Glu	Cys 1090		Суз	Ser	Ala	Val 1095		Ser	Tyr	Ala	Gln 110		Cys	Thr	Lys
Glu 1105		Ala	Cys	Val	Phe 1110		Arg	Thr	Pro	Asp 111!		Cys	Pro	Ile	Phe 1120
Суз	Asp	Tyr	Tyr	Asn 112		Pro	His	Glu	Cys 113	Glu O	Trp	His	Tyr	Glu 1135	
Cys	Gly	Asn	Arg 1140		Phe	Glu	Thr	Cys 1145	_	Thr	Ile	Asn	Gly 1150		His
Ser	Asn	Ile 1155		Val	Ser	Tyr	Leu 1160		Gly	Cys	Tyr	Pro 1165		Cys	Pro
Lys	Asp 1170		Pro	Ile	Tyr	Glu 1175		Asp	Leu	Lys	Lys 1180	_	Val	Thr	Ala
Asp 1185	_	Суз	Gly	Суз	Tyr 1190		Glu	Asp	Thr	His 119	_	Pro	Pro	Gly	Ala 1200

Ser Val Pro Thr Glu Glu Thr Cys Lys Ser Cys Val Cys Thr Asn Ser 1205 1210 1215

- Ser Gln Val Val Cys Arg Pro Glu Glu Gly Lys Ile Leu Asn Gln Thr 1220 1225 1230
- Gln Asp Gly Ala Phe Cys Tyr Trp Glu Ile Cys Gly Pro Asn Gly Thr 1235 1240 1245
- Val Glu Lys His Phe Asn Ile Cys Ser Ile Thr Thr Arg Pro Ser Thr 1250 1255 1260
- Leu Thr Thr Phe Thr Thr Ile Thr Leu Pro Thr Thr Pro Thr Ser Phe 1265 1270 1275 1280
- Thr Thr Thr Thr Thr Thr Thr Pro Thr Ser Ser Thr Val Leu Ser
 1285 1290 1295
- Thr Thr Pro Lys Leu Cys Cys Leu Trp Ser Asp Trp Ile Asn Glu Asp 1300 1305 1310
- His Pro Ser Ser Gly Ser Asp Asp Gly Asp Arg Glu Pro Phe Asp Gly 1315 1320 1325
- Val Cys Gly Ala Pro Glu Asp Ile Glu Cys Arg Ser Val Lys Asp Pro 1330 1335 1340
- His Leu Ser Leu Glu Gln His Gly Gln Lys Val Gln Cys Asp Val Ser 1345 1350 1355 1360
- Val Gly Phe Ile Cys Lys Asn Glu Asp Gln Phe Gly Asn Gly Pro Phe 1365 1370 1375
- Gly Leu Cys Tyr Asp Tyr Lys Ile Arg Val Asn Cys Cys Trp Pro Met 1380 1385 1390
- Asp Lys Cys Ile Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ser Pro 1395 1400 1405
- Pro Pro Thr Thr Thr Thr Leu Pro Pro Thr Thr Pro Ser Pro 1410 1415 1420
- Pro Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro 1425 1430 1435 1446
- Pro Ile Thr Thr Thr Thr Pro Leu Pro Thr Thr Pro Ser Pro 1445 1450 1455
- Pro Ile Ser Thr Thr Thr Pro Pro Pro Thr Thr Pro Ser Pro 1460 1465 1470
- Pro Thr Thr Pro Ser Pro Pro Thr Thr Pro Ser Pro Pro Thr 1475 1480 1485
- Thr Thr Thr Thr Pro Pro Pro Thr Thr Pro Ser Pro Pro Met 1490 1495 1500

Thr Thr Pro Ile Thr Pro Pro Ala Ser Thr Thr Thr Leu Pro Pro Thr 1505 1510 1515 1520

Thr Thr Pro Ser Pro Pro Thr Thr Thr Thr Thr Pro Pro Pro Thr 1525 1530 1535

Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ile Thr Pro Pro Thr Ser 1540 1545 1550

Thr Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr 1555 1560 1565

Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr 1570 1580

Thr Pro Ser Pro Pro Thr Ile Thr Thr Thr Thr Pro Pro Pro Thr Thr 1585 1590 1595 1600

Thr Pro Ser Pro Pro Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr 1605 1610 1615

Thr Pro Ser Pro Pro Thr Thr Pro Ile Thr Pro Pro Thr Ser Thr 1620 1625 1630

Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr Thr 1635 1640 1645

Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr 1650 1655 1660

Pro Ser Pro Pro Ile Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr 1665 1670 1675 1680

Pro Ser Ser Pro Ile Thr Thr Thr Pro Ser Pro Pro Thr Thr Met
1685 1690 1695

Thr Thr Pro Ser Pro Thr Thr Thr Pro Ser Ser Pro Ile Thr Thr Thr 1700 1705 1710

Thr Thr Pro Ser Ser Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr Met 1715 1720 1725

Thr Thr Pro Ser Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Met 1730 1735 1740

Thr Thr Leu Pro Pro Thr Thr Ser Ser Pro Leu Thr Thr Thr Pro 1745 1750 1755 1760

Leu Pro Pro Ser Ile Thr Pro Pro Thr Phe Ser Pro Phe Ser Thr Thr 1765 1770 1775

Thr Pro Thr Thr Pro Cys Val Pro Leu Cys Asn Trp Thr Gly Trp Leu 1780 1785 1790

Asp Ser Gly Lys Pro Asn Phe His Lys Pro Gly Gly Asp Thr Glu Leu 1795 1800 1805

Ile Gly Asp Val Cys Gly Pro Gly Trp Ala Ala Asn Ile Ser Cys Arg

	1810)				1815	,				1820)			
Ala 1825		Met	Tyr	Pro	Asp 1830	Val	Pro	Ile	Gly	Gln 1835		Gly	Gln	Thr	Val 1840
Val	Cys	Asp	Val	Ser 1845		Gly	Leu	Ile	Cys 1850		Asn	Glu	Asp	Gln 1855	
Pro	Gly	Gly	Val 1860		Pro	Met	Ala	Phe 1865	-	Leu	Asn	Tyr	Glu 1870		Asn
Val	Gln	Cys 1875		Glu	Суз	Val	Thr 1880		Pro	Thr	Thr	Met 1885		Thr	Thr
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Arg Asn Trp Ser Asp Ala Glu Leu Glu Cys Gln Ser Tyr Gly Asn Gly

55

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Ala His Leu Ala Ser Ile Leu Ser Leu Lys Glu Ala Ser Thr Ile Ala 65 70 75 80

Glu Tyr Ile Ser Gly Tyr Gln Arg Ser Gln Pro Ile Trp Ile Gly Leu 85 90 95

His Asp Pro Gln Lys Arg Gln Gln Trp Gln Trp Ile Asp Gly Ala Met
100 105 110

Tyr Leu Tyr Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His 115 120 125

Cys Ala Glu Met Ser Ser Asn Asn Asn Phe Leu Thr Trp Ser Ser Asn 130 135 140

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35 40 45

Arg Asn Trp Ser Asp Ala Glu Leu Glu Cys Gln Ser Tyr Gly Asn Gly 50 60

Ala His Leu Ala Ser Ile Leu Ser Leu Lys Glu Ala Ser Thr Ile Ala 65 70 75 80

Glu Tyr Ile Ser Gly Tyr Gln Arg Ser Gln Pro Ile Trp Ile Gly Leu 85 90 95

His Asp Pro Gln Lys Arg Gln Gln Trp Gln Trp Ile Asp Gly Ala Met
100 105 110

Tyr Leu Tyr Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His
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Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile

Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly

Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr

Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val

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Gly	Gln	Leu	Tyr	Tyr 165	Gln	Ile	Val	Ile	Gln 170	Leu	Pro	Met	Ile	Asn 175	Asn
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Arg	Glu	Gly 195	Ser	Gln	Glu	Leu	Asn 200	Pro	Ala	Lys	Asn	Pro 205	Ser	Tyr	Asn
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Ala	Pro	Lys	Pro	Val 245	Glu	Met	Val	Glu \	Asn 250	Ser	Thr	Asp	Pro	His 255	Pro
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Trp	Leu 610	Lys	Ile	Asp	His	Val 615	Thr	Gly	Glu	Ile	Phe 620	Ser	Val	Ala	Pro
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